

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2005, 19:45:33 ; Search time 8237 Seconds
(without alignments)
1147.582 Million cell updates/sec

Title: US-09-559-013E-23

Perfect score: 1895
Sequence: 1 gtagagggcgtgtgtcc.....tgtgtatctcaaaaaaaaa 1895

Scoring table: OLIGO_NUC
Gapop_60.0, Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size: 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database:

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1886	99.5	1886	9	AB051833 Homo sapi
2	1780	94.5	1899	9	BC033010 Homo sapi
3	1742	91.9	1912	6	BD268022 Proteasas
4	1742	91.9	1912	6	BD192303 Secreted
5	1284	78.8	1899	6	BD136402 95 human
6	1284	78.8	1899	6	BD136402 95 human
7	719	37.9	2299	6	CQ722423 Sequence
8	528	27.9	964	6	BD139445 Extended
9	471	24.9	56580	2	AC135892 Homo sapi
10	471	24.9	245880	2	AC079387 Homo sapi
11	281	17.9	516	6	HDMP2A2A04
12	281	17.9	516	6	HDMP2A2A04
13	280	14.8	507	6	BD060281 Secreted
14	280	14.8	507	6	BD060281 Secreted
15	149	7.9	391	11	BD179034 Cancer as
16	149	7.9	391	11	BD179034 Cancer as
17	112	5.9	128	6	AX968632 Sequence
18	112	5.9	128	6	AX968632 Sequence
19	71	3.7	316	6	AR415759 Sequence
20	71	3.7	316	6	AX972593 Sequence
21	71	3.7	316	6	BD111312 EST and e

20	60	3.2	60	6	CQ552626 Sequence
21	46	2.4	1813	4	PIGACRSN
22	46	2.4	1813	4	MUSP32A
23	46	2.4	166392	10	AC134529
24	34	1.8	261384	2	AC115415
25	32	1.7	1880	10	GPACRSN
26	27	1.4	29	6	BD192313 Secreted
27	26	1.4	1284	10	BC079212
28	24	1.3	66985	2	AC127516
29	24	1.3	67078	2	AC100227
30	24	1.3	156599	2	AC083840
31	24	1.3	190809	9	AC129908
32	24	1.3	198895	2	AP001337
33	24	1.3	204584	10	AC122243
34	24	1.3	204623	2	AP001338
35	24	1.3	215127	10	AC113542
36	24	1.3	215676	2	AC131299
37	24	1.3	221944	2	AC119914
38	23	1.2	2941	5	BC047248
39	23	1.2	2941	5	XL085969
40	23	1.2	2947	5	BC074454
41	23	1.2	198392	10	AL603745
42	23	1.2	225503	2	AC112301
43	23	1.2	231912	2	AC087566
44	23	1.2	232717	2	AC094171
45	23	1.2	234746	10	CNS080CAS
46	22	1.2	658	10	BC061122
47	22	1.2	1253	10	MUSP32B
48	22	1.2	1524	10	BC011079
49	22	1.2	1638	11	BV007555
50	22	1.2	28124	8	AP006410
51	22	1.2	67573	2	AC122760
52	22	1.2	100559	8	ATAC018363
53	22	1.2	112104	2	AC140155
54	22	1.2	124236	10	AL935312
55	22	1.2	173358	2	AC145050
56	22	1.2	175552	10	AC101691
57	22	1.2	181066	2	AC144606
58	22	1.2	183707	2	AY178785
59	22	1.2	184088	10	AC109305
60	22	1.2	184577	10	AC101728
61	22	1.2	193725	10	AC121575
62	22	1.2	198374	2	AC118519
63	22	1.2	200368	9	AC096541
64	22	1.2	215816	2	AC134937
65	22	1.2	222938	2	AC095075
66	22	1.2	226225	2	AC121002
67	22	1.2	236871	2	AC114108
68	22	1.2	251550	2	AC133772
69	22	1.2	259204	2	AC095370
70	22	1.2	299543	2	AC106692
71	21	1.1	450	6	AX778819
72	21	1.1	1053	4	AB075899
73	21	1.1	2411	6	AB075899
74	21	1.1	2435	9	HSMTM1
75	21	1.1	2450	9	HSMTM1
76	21	1.1	2525	5	BC067984
77	21	1.1	2684	9	BC019311
78	21	1.1	27645	10	AB075899
79	21	1.1	47300	9	HSMTM1
80	21	1.1	47405	2	AC136789
81	21	1.1	55516	2	AC101274
82	21	1.1	59767	6	CO870186
83	21	1.1	76982	9	AL731552
84	21	1.1	82082	8	AP006394
85	21	1.1	109092	10	AL928803
86	21	1.1	112354	2	AC101605
87	21	1.1	125922	9	AL731566
88	21	1.1	134482	2	AC007335
89	21	1.1	145208	2	AC132921
90	21	1.1	153192	9	HSMTM1
91	21	1.1	158383	2	AC140161
92	21	1.1	158972	2	CR752649

Accession	Species	Accession	Species	Accession	Species	Accession	Species	Accession	Species						
C 93	21	1.1	161419	2	AC136927	AC136927	Homo sapi	C 166	20	1.1	7362	6	AR022379	AR022379	Sequence
C 94	21	1.1	16719	9	AC136957	AC136957	Homo sapi	C 167	20	1.1	7362	6	AR063882	AR063882	Sequence
C 95	21	1.1	172280	9	AC1390879	AC1390879	Human DNA	C 168	20	1.1	7362	6	AR067882	AR067882	Sequence
C 96	21	1.1	173595	9	AC1402766	AC1402766	Homo sapi	C 169	20	1.1	7362	6	AR105183	AR105183	Sequence
C 97	21	1.1	174452	2	AC142369	AC142369	Homo sapi	C 170	20	1.1	7362	6	AR138608	AR138608	Sequence
C 98	21	1.1	175199	10	AL844480	AL844480	Mouse DNA	C 171	20	1.1	7364	6	AR138608	AR138608	Sequence
C 99	21	1.1	175465	2	AL356783	AL356783	Homo sapi	C 172	20	1.1	7364	6	AR138608	AR138608	Sequence
C 100	21	1.1	176290	10	AC145454	AC145454	Homo sapi	C 173	20	1.1	7364	6	AR138608	AR138608	Sequence
C 101	21	1.1	176290	2	AC145454	AC145454	Homo sapi	C 174	20	1.1	7364	6	AR138608	AR138608	Sequence
C 102	21	1.1	180424	2	AC148564	AC148564	Papio anu	C 175	20	1.1	7366	6	AR138608	AR138608	Sequence
C 103	21	1.1	185895	2	AC150732	AC150732	Mus muscu	C 176	20	1.1	7366	6	AR138608	AR138608	Sequence
C 104	21	1.1	188394	2	AC150732	AC150732	Mus muscu	C 177	20	1.1	7366	6	AR138608	AR138608	Sequence
C 105	21	1.1	191886	9	AC150732	AC150732	Mus muscu	C 178	20	1.1	7366	6	AR138608	AR138608	Sequence
C 106	21	1.1	19434	9	AC150732	AC150732	Mus muscu	C 179	20	1.1	7366	6	AR138608	AR138608	Sequence
C 107	21	1.1	199204	2	AC150732	AC150732	Mus muscu	C 180	20	1.1	7366	6	AR138608	AR138608	Sequence
C 108	21	1.1	202234	2	AC150732	AC150732	Mus muscu	C 181	20	1.1	7366	6	AR138608	AR138608	Sequence
C 109	21	1.1	207232	2	AC150732	AC150732	Mus muscu	C 182	20	1.1	7366	6	AR138608	AR138608	Sequence
C 110	21	1.1	207232	2	AC150732	AC150732	Mus muscu	C 183	20	1.1	7366	6	AR138608	AR138608	Sequence
C 111	21	1.1	207232	2	AC150732	AC150732	Mus muscu	C 184	20	1.1	7366	6	AR138608	AR138608	Sequence
C 112	21	1.1	209336	10	AC150732	AC150732	Mus muscu	C 185	20	1.1	7366	6	AR138608	AR138608	Sequence
C 113	21	1.1	211815	2	CR753872	CR753872	Mus muscu	C 186	20	1.1	7366	6	AR138608	AR138608	Sequence
C 114	21	1.1	213290	5	CR753872	CR753872	Mus muscu	C 187	20	1.1	7366	6	AR138608	AR138608	Sequence
C 115	21	1.1	214202	2	AC123624	AC123624	Mus muscu	C 188	20	1.1	7366	6	AR138608	AR138608	Sequence
C 116	21	1.1	215435	2	AC123624	AC123624	Mus muscu	C 189	20	1.1	7366	6	AR138608	AR138608	Sequence
C 117	21	1.1	232410	2											

us-09-559-013e-23.res

Page 2

GCCACTCAGAGGCCA-GCCTCAGCGGC-AACAATGGCACACTCCCAAGAAGCT-CCCTTGTACGCCCT
 |||||
 GCTCTC-AGCGCAGGCTCTGGAAGGCTCGGCTGTCTGTACCTGAAGTGGGGGTAGATGGGGAGGTCTAT
 |||||
 430 440 450 460 470 480 490
 TGCCTGCTCCAGAGCTCTCTCATCGGCAACAGTAAAGGCTCCCAAGATCAAGGCGCTTTTACGGGCTGG
 |||||
 --CGTG-GTGGGTAAAGT-TC-AAGCTG-AAGCTCTTA---TCTCTT X
 |||||
 500 510 520
 1350 1360
 ATTGTACGGTGGGCTCCACATGGAC

> 0 <
0 | 0 InelliGenetics
> 0 <

GENALIGN - Multiple Sequence Alignment Program Release 5.4

Wed 9 Mar 105 16:01:59- PST

Solution Parameters:

Nucleic Alphabet = Identity
Output line length = 80
Compress = Off
Histogram = Off
Randomization = Off

AMINO-Res-length = 2
Deletion-weight = 5.00
Length-factor = 0
Matching-weight = 1.00
NUCLEIC-Res-length = 4
Spread-factor = 50

Clustered order of selected sequences:

13. US-09-559-013E-23 (1-1895)
23. US-09-559-013E-33 (1-529)

Region Alignment: (listed in clustered order)

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US-09-559- 1 gtagagcgcgctgtgtccagcgagcgcgcgatctctccgcatgaggaagccag
US-09-559- 1
US-09-559- 62 ccgctggcttcctccctcaactctgaagtgtcgtccctcctcgcaactgcgagc
US-09-559- 1
consensus  ccgctggcttcctccctcaactctgaagtgtcgtccctcctcgcaactgcgagc
US-09-559- 123 ccaggaatcgaaatccagcccccaactccagcagccctctctcctaccgaatacgaagc
US-09-559- 1
consensus  ccaggaatcgaaatccagcccccaactccagcagccctctctcctaccgaatacgaagc
US-09-559- 184 tcttcgcgaactgtgaactccaactggaagcagaagactacgtcgtctccgtcgcgcaacc
US-09-559- 1
consensus  tcttcgcgaactgtgaactccaactggaagcagaagactacgtcgtcgcgcaacc
US-09-559- 245 acggctgcggaaatcccaactcgtccagctggaaccaatagaaaacacggcttaagtc
US-09-559- 1
consensus  acggctgcggaaatcccaactcgtccagctggaaccaatagaaaacacggcttaagtc
US-09-559- 306 cgatgctgctgtcgtcctcaaccccttaagctcctcctgagtccttctcgcagctc
US-09-559- 1
consensus  cgatgctgctgtcgtcctcaaccccttaagctcctcctgagtccttctcgcagctc

```

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US-09-559- 367 actcaccacgctgtctccaaacacgctcactatccaaagagtcctgtgttccacgacg
US-09-559- 9          CTCCA          gTAgagttctcAtcatatTTcAtcatctt
consensus  actcaccacgctgtctccaaacacgctcactatccaaagagtcctgtgttccacgacg
US-09-559- 428 tctcTATTctctcaactcaacatctcaaggatagaagcttcagctgaagctcaccac
US-09-559- 46 catctATT
consensus  --TCTATTctctcaactcaacatctcaaggatagaagcttcagctgaagctcaccac
US-09-559- 489 cagatgaactcccccatctcaccacatccacagtgacagaacgccaacctccagcc
US-09-559- 54          tcc
consensus  cagatgaactcccccatctcaccacatccacagtgacagaacgccaacctccagcc
US-09-559- 550 TGcCTGAagaggtccagcaacaaacgtcgaAAGACTCTTacaatcctTcgtCctTgggAg
US-09-559- 57 TGcGCTGA          tcdAtGAGCTCCT          ggAtgtTctcCAtTatcAt
consensus  TGc-CTGAagaggtccagcaacaaac--G-A-GAGCTCCTacaaa--T--T--C--T--A-
US-09-559- 611 gccAGAGcaagcgcCagagacagaagAGAGAGaggtgagacaagagcgagccgac
US-09-559- 98 aggAGtAGactctatctctcgtaaccggGGAGCAA
consensus  ---AG-AG-----C-----GAGAGAGaggtgagacagagcagagccgac
US-09-559- 672 acaagaacacacagcaggaagaggggcagaaacagaagagcaAGAGAGAGaggaag
US-09-559- 133          AAGAGAGAA
consensus  acaagaacacacagcaggaagaggggcagaaacagaagagcaAGAGAGAGaggaag
US-09-559- 733 gagggaaagcagAGAGAGacaggggactaaggaggagcggtgtgtcctcagctgc
US-09-559- 141          ggGtTAGAAG
consensus  gagggaaag--G--AGAGAGacaggggactaaggaggagcggtgtgtcctcagctgc
US-09-559- 794 AGAcAGACTCAGAGcCCAGTTTcACTCTGAtctctatcttctaaccctcctcttgc
US-09-559- 151 AtAGAGAtTCAGAtgaaAaCTTggCTTGA
consensus  A-A-AGA-TCAGAG--AA-TT--CTCTGAtctctatcttctaaccctcctcttgc
US-09-559- 855 tccccggtaacagaaatagaGTTactcctatgataatgagaacatccagagctccat
US-09-559- 182          GTCT
consensus  tccccggtaacagaaatagaGTTactcctatgataatgagaacatccagagctccat
US-09-559- 916 cgatcagccaggaatagatgaaatgaatgaatgatgatgagaactcctactggaaga
US-09-559- 186          cgatcagccaggaatagatgaaatgaatgaatgatgatgagaactcctactggaaga
consensus  cgatcagccaggaatagatgaaatgaatgaatgatgatgagaactcctactggaaga
US-09-559- 977 accaaaaacctggcagcttctGcAGCTGcccccACAGAGagggccttgctgtgtgcta

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US-09-559- 186          SECTGCACTG  AGACACAG
consensus      accaaaacctggcagct--CTGCAGCTGcc--ACACAGagcccttgctgctgctga

US-09-559- 1038  ttcgacccgctggagaaTAcCTgcacTataacCCcCaagcCcaagcCtTgaagTacaTggag
US-09-559- 205      cctccGctccctcTtagTccCctcgtCcttccTccTccgtcttCcctccctccctcct
consensus      ttcg-----G-----T-C-T-----C-----CC-----C-----C-----G--

US-09-559- 1099  gaagagatTccttgTttccGgaagtGgctcTgTgaagcctTgGcgGcgagacaatgCTa
US-09-559- 262  cctctcttgctcctcctGctGctcTgCccctcctccctcgtGcttGcttGctcgtcCTg
consensus      -----T--T--T--G-----C-----T-----TG--C-----CT--

US-09-559- 1160  CCTGTGccctcTgTgaacttcTGcTCCTTgaagctggagcagcagTCaCTcaagagccagCCT
US-09-559- 323  CCTGTGc      TccactcctTGCTCTT      gcttGTC      tctggcgcttgctcCT
consensus      CCTGTGccctcT-----TGCTCCTTgaagctgG---GTGCC-CT-----CCT--

US-09-559- 1221  GcagcgGcaacaatgcagacactcccaagaagactcccttgtcagcccttgcttGCTCC
US-09-559- 370  G                                GCTTCC
consensus      GcagcgGcaacaatgcagacactcccaagaagactcccttgtcagcccttgcttGCTCC

US-09-559- 1282  CAGagccttgctccAtcGcGAaccagGTAGggtcccccAGaAacagCCGcCTTcaCGgctGg
US-09-559- 377  CAG      ggAcaagGAggattGTAGG      AgctcttCCaGgTgTtGctGgc
consensus      CAGagcctgT--A---G-A-----GTAGggtcccccagA-----CC-C-TT---G---G-

US-09-559- 1343  aTtTgtaGgTgGGCTccacatGgActTGTGctgTgcccGgcttGcCaGaaagCTGTGA
US-09-559- 423  ctTcTcaGgccaGgGcT      gGaAggTCTGG      GgttcTgTcaCTGTGA
consensus      -T-T-----GGGCTTccaca-G-A--TCTGctgTgcccGgcttGc-----CTGTGA

US-09-559- 1404  AGatgtccgagctctcTGGGtgctccagactgagcttccttagcttccagGATGGGaatTtc
US-09-559- 466  AG      tggGGTg      aGATGGG
consensus      AGatgtccgagctcT--GGGTgctccagactgagcttccttagcttcca-GATGGGaatTtc

US-09-559- 1465  cctacaagatltgtgacacagactatattccagtaaccaactactgltcccttcaaaagcc
US-09-559- 483
consensus      cctacaagatltgtgacacagactatattccagtaaccaactactgltcccttcaaaagcc

US-09-559- 1526  agcagtgTcTgtaTgagaacCGcAATCGaagGTGtcccgcatgagatgTctgCagaatTGA
US-09-559- 483      gagGtcATCG      tGGTg      gGTGA
consensus      agcagtgTcTgtaTgagaa---G--ATCGga-GGTGtcccgcatgagatgTctgCag--TGA

US-09-559- 1587  GACTTAcagTgcgctgagccctggcaaaagtgaagacgttgTgcttcatgagTgagccagagag
US-09-559- 503  GACTT
consensus      GACTTAcagTgcgctgagccctggcaaaagtgaagacgttgTgcttcatgagTgagccagagag

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US-09-559- 1648  ttcagacacttgactctaagccaggtcgagTAgCTGcggtctatctctgcccacaccag
US-09-559- 508      |||||
consensus      ttcagacacttgactctaagccaggtcggat-AGCTGcggtctatctctgcccacaccag

US-09-559- 1709  cccaacctggcccaagttcTATgTtcttgagaccccatgcttcaagctgccccctcTg
US-09-559- 514      |||||
consensus      cccaacctggccca-----TCTATgTtcttgagaccccatgcttcaagctgccccctcTg

US-09-559- 1770  gTctcgttactcgccctactacatltccttggTtggagcaacagTcccagaagggc
US-09-559- 524
consensus      gTctcgttactcgccctactacatltccttggTtggagcaacagTcccagaagggc

US-09-559- 1831  caGgTgGgagctgcgcCCTCCTTaaagatgacttacaTaaatgtgatcttcaaaaa
US-09-559- 524      |||||
consensus      caGgTgGgagctgcgcCCTCCTTaaagatgacttacaTaaatgtgatcttcaaaaa

US-09-559- 1892  aaaa
US-09-559- 530
consensus      aaaa

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Alignment score = -6577.00

Scoring matrix:

13	-6643
23	13 23

239	20	1.1	174952	9	AC002460	AC002460 Human BAC	C 312	20	1.1	238861	2	AC148331	AC148331 Mus muscu
C 240	20	1.1	175251	2	AC101838	AC101838 Mus muscu	313	20	1.1	240584	2	AC116063	AC116063 Rattus no
241	20	1.1	175302	9	AL355677	AL355677 Human DNA	C 314	20	1.1	241086	2	AC106653	AC106653 Rattus no
C 242	20	1.1	175360	2	AC018948	AC018948 Homo sapi	C 315	20	1.1	242195	2	AC126644	AC126644 Rattus no
243	20	1.1	175491	2	AC129683	AC129683 Rattus no	C 316	20	1.1	242510	2	AC128507	AC128507 Rattus no
C 244	20	1.1	175639	10	AC132557	AC132557 Mus muscu	C 317	20	1.1	243306	2	AC130628	AC130628 Rattus no
C 245	20	1.1	176372	2	AC026030	AC026030 Homo sapi	C 318	20	1.1	244451	2	AC125765	AC125765 Rattus no
C 246	20	1.1	176889	10	AC124830	AC124830 Mus muscu	C 319	20	1.1	245496	10	AC125765	AC125765 Rattus no
C 247	20	1.1	176915	9	AC008050	AC008050 Homo sapi	C 320	20	1.1	245971	2	AC133446	AC133446 Rattus no
C 248	20	1.1	177115	9	AC091805	AC091805 Homo sapi	C 321	20	1.1	249068	2	AC095295	AC095295 Rattus no
C 249	20	1.1	177483	9	AC068233	AC068233 Homo sapi	C 322	20	1.1	250688	2	AC094683	AC094683 Rattus no
250	20	1.1	177952	10	AC113033	AC113033 Mus muscu	C 323	20	1.1	251186	2	AC120750	AC120750 Rattus no
C 251	20	1.1	178380	2	AC129819	AC129819 Rattus no	C 324	20	1.1	251194	2	AC103307	AC103307 Rattus no
252	20	1.1	178523	8	AC135561	AC135561 Oryza sat	C 325	20	1.1	253149	2	AC107527	AC107527 Rattus no
253	20	1.1	182071	9	AC103740	AC103740 Homo sapi	C 326	20	1.1	254452	2	AC118338	AC118338 Rattus no
254	20	1.1	183577	2	AC011164	AC011164 Homo sapi	C 327	20	1.1	254646	2	AC109890	AC109890 Rattus no
C 255	20	1.1	184365	2	AC079639	AC079639 Mus muscu	C 328	20	1.1	255239	2	AC109676	AC109676 Rattus no
C 256	20	1.1	184738	9	AL162574	AL162574 Human DNA	C 329	20	1.1	256229	2	AC073676	AC073676 Mus muscu
C 257	20	1.1	185855	5	CR759734	CR759734 Zebrafish	C 330	20	1.1	269739	10	AC139108	AC139108 Mus muscu
C 258	20	1.1	186205	10	AC140336	AC140336 Mus muscu	C 331	20	1.1	271600	2	AC107601	AC107601 Rattus no
C 259	20	1.1	186330	9	AC007376	AC007376 Homo sapi	C 332	20	1.1	271932	2	AC109948	AC109948 Rattus no
C 260	20	1.1	187540	2	AC126669	AC126669 Mus muscu	C 333	20	1.1	289782	2	AC151297	AC151297 Mus muscu
261	20	1.1	189091	2	AC118207	AC118207 Mus muscu	C 334	20	1.1	290248	2	AC094662	AC094662 Rattus no
C 262	20	1.1	189924	2	AC119933	AC119933 Mus muscu	C 335	20	1.1	293412	2	AC133037	AC133037 Rattus no
C 263	20	1.1	190853	5	BX005041	BX005041 Zebrafish	C 336	20	1.1	313096	2	AC113536	AC113536 Mus muscu
264	20	1.1	192169	2	AC020849	AC020849 Mus muscu	C 337	20	1.1	337636	2	AE003584	AE003584 Drosophila
265	20	1.1	192619	2	AC122789	AC122789 Mus muscu	C 338	20	1.1	349980	6	AX781290	AX781290 Sequence
C 266	20	1.1	193212	9	AP004370	AP004370 Homo sapi	C 339	19	1.0	352	3	AY619275	AY619275 Daphnia p
C 267	20	1.1	193380	2	AC013730	AC013730 Homo sapi	C 340	19	1.0	367	6	AX916154	AX916154 Sequence
C 268	20	1.1	193939	2	AC113413	AC113413 Homo sapi	C 341	19	1.0	367	6	BD051687	BD051687 Sequence
C 269	20	1.1	194792	9	AC115931	AC115931 Mus muscu	C 342	19	1.0	378	6	CQ448501	CQ448501 Sequence
270	20	1.1	194937	9	BS000153	BS000153 Pan trogl	C 343	19	1.0	383	8	AF543707	AF543707 Botryosph
C 271	20	1.1	195742	2	AC151362	AC151362 Ictalurus	C 344	19	1.0	472	6	CQ698065	CQ698065 Sequence
272	20	1.1	196272	2	AC026675	AC026675 Homo sapi	C 345	19	1.0	530	8	AF484753	AF484753 Temarix p
273	20	1.1	196773	10	AC023613	AC023613 Mus muscu	C 346	19	1.0	578	8	AB065389	AB065389 F11obasid
274	20	1.1	197131	2	AC121829	AC121829 Mus muscu	C 347	19	1.0	580	6	AR412990	AR412990 Sequence
275	20	1.1	199519	10	AC121872	AC121872 Mus muscu	C 348	19	1.0	580	6	AX969824	AX969824 Sequence
C 276	20	1.1	200222	2	AC023555	AC023555 Homo sapi	C 349	19	1.0	603	6	BD108543	BD108543 EST and e
277	20	1.1	200265	2	AC099579	AC099579 Mus muscu	C 350	19	1.0	603	6	BD10354	BD10354 Human gen
278	20	1.1	200465	2	AC148786	AC148786 Oryzomys	C 351	19	1.0	634	11	G91812	G91812 S208P6788RE
279	20	1.1	202141	2	BX957272	BX957272 Danio rer	C 352	19	1.0	645	10	AY055379	AY055379 Rattus no
C 280	20	1.1	203159	10	AC137525	AC137525 Mus muscu	C 353	19	1.0	760	3	PMH1582B	PMH1582B Rattus no
281	20	1.1	203974	2	BX914220	BX914220 Danio rer	C 354	19	1.0	845	5	SUPH15B2	SUPH15B2 F.miliaris
C 282	20	1.1	204428	2	AC138019	AC138019 Papio anu	C 355	19	1.0	930	5	AF294666	AF294666 Heliomast
C 283	20	1.1	205580	2	AC101839	AC101839 Mus muscu	C 356	19	1.0	930	5	AF294667	AF294667 Hylochari
C 284	20	1.1	207080	2	AC146149	AC146149 Pan trogl	C 357	19	1.0	930	5	AY065759	AY065759 Galliaris
285	20	1.1	209454	2	CR626940	CR626940 Danio rer	C 358	19	1.0	930	5	AY065750	AY065750 Hylopezus
C 286	20	1.1	211414	2	AC150057	AC150057 Gallus ga	C 359	19	1.0	930	5	AY339102	AY339102 Arenaria
287	20	1.1	211555	2	AC132172	AC132172 Rattus no	C 360	19	1.0	930	5	AY339114	AY339114 Phalaropa
288	20	1.1	211595	2	AC019334	AC019334 Homo sapi	C 361	19	1.0	930	5	AY339124	AY339124 Thinnocoru
289	20	1.1	211786	2	AC135516	AC135516 Rattus no	C 362	19	1.0	930	5	AY339125	AY339125 Tringa to
290	20	1.1	213085	2	AC095379	AC095379 Rattus no	C 363	19	1.0	945	6	CQ737551	CQ737551 Sequence
C 291	20	1.1	213683	10	AC109280	AC109280 Mus muscu	C 364	19	1.0	963	6	AX576131	AX576131 Sequence
292	20	1.1	213779	2	AC113958	AC113958 Mus muscu	C 365	19	1.0	1107	5	GGLAMP99	GGLAMP99 G.gallus nr
293	20	1.1	213817	2	AC099865	AC099865 Mus muscu	C 366	19	1.0	1247	5	CR523041	CR523041 Gallus ga
C 294	20	1.1	215101	2	AC148847	AC148847 Oryzomys	C 367	19	1.0	1287	6	AR429815	AR429815 Sequence
C 295	20	1.1	215175	2	AC108664	AC108664 Rattus no	C 368	19	1.0	1289	8	AK071491	AK071491 Oryza sat
C 296	20	1.1	215449	2	AL590654	AL590654 Mus muscu	C 369	19	1.0	1364	8	AF458274	AF458274 Tritlicum
C 297	20	1.1	218644	9	AC147079	AC147079 Pan trogl	C 370	19	1.0	1383	3	SPH2B01	SPH2B01 Sea urchin
C 298	20	1.1	219486	2	AC116283	AC116283 Rattus no	C 371	19	1.0	1521	6	AR429826	AR429826 Sequence
C 299	20	1.1	221608	2	AC135934	AC135934 Rattus no	C 372	19	1.0	1632	9	AK024786	AK024786 Homo sapi
C 300	20	1.1	223352	10	AC107742	AC107742 Mus muscu	C 373	19	1.0	1713	6	AR375702	AR375702 Sequence
C 301	20	1.1	225930	2	AC150170	AC150170 Gallus ga	C 374	19	1.0	1729	8	AB088027	AB088027 Camellia
302	20	1.1	233772	2	AC115403	AC115403 Rattus no	C 375	19	1.0	1730	6	B39318	B39318 beta-Primev
C 303	20	1.1	234362	2	AC114567	AC114567 Mus muscu	C 376	19	1.0	1731	6	BD180525	BD180525 Highly th
C 304	20	1.1	234717	2	AC095154	AC095154 Rattus no	C 377	19	1.0	1914	5	AF294683	AF294683 Trachypno
C 305	20	1.1	235326	2	AC105692	AC105692 Rattus no	C 378	19	1.0	1914	5	AF294684	AF294684 Staccolae
C 306	20	1.1	235794	2	AC151298	AC151298 Mus muscu	C 379	19	1.0	1914	5	AF295195	AF295195 Picumnus
307	20	1.1	235868	10	AL645947	AL645947 Mouse DNA	C 380	19	1.0	1934	5	AY165794	AY165794 Indicator
C 308	20	1.1	236010	2	AC151268	AC151268 Mus muscu	C 381	19	1.0	1934	5	AK026807	AK026807 Homo sapi
C 309	20	1.1	236951	2	AC098662	AC098662 Rattus no	C 382	19	1.0	1949	10	BC029741	BC029741 Mus muscu
310	20	1.1	237720	2	AC132559	AC132559 Rattus no	C 383	19	1.0	1951	5	BC049336	BC049336 Danio rer
C 311	20	1.1	238390	2	AC117035	AC117035 Rattus no	C 384	19	1.0	2000	6	AX461161	AX461161 Sequence

C 385	19	1.0	2000	6	AX508752	Sequence	458	19	1.0	9743	14	AF435866	AF435866 Rubella v
C 386	19	1.0	2011	10	AB039933	Mus muscu	459	19	1.0	9755	14	RUBCG	M15240 Rubella v
C 387	19	1.0	2017	14	AF231105	VP1356 Sea urchin	460	19	1.0	9759	6	IC3470	IC3470 Sequence 1
C 388	19	1.0	2033	3	SPHIS1	AB061073 Drosophila	461	19	1.0	9762	14	AB047329	AB047329 Rubella v
C 389	19	1.0	2043	3	BC064942	AK000743 Homo sapi	462	19	1.0	9762	14	AB047330	AB047330 Rubella v
C 390	19	1.0	2190	3	BC064942	AK000743 Homo sapi	463	19	1.0	9762	14	AB047330	AB047330 Rubella v
C 391	19	1.0	2228	6	AK000743	BC084637 Xenopus laevis	464	19	1.0	9762	14	AB047330	AB047330 Rubella v
C 392	19	1.0	2236	6	BC084637	BC084637 Xenopus laevis	465	19	1.0	9762	14	AB047330	AB047330 Rubella v
C 393	19	1.0	2305	5	AB052096	AY118334 Drosophila	466	19	1.0	13415	9	AC079087	AC079087 Homo sapi
C 394	19	1.0	2325	9	AB052096	AY118334 Drosophila	467	19	1.0	13415	9	AC079087	AC079087 Homo sapi
C 395	19	1.0	2352	3	AY118334	AY118334 Drosophila	468	19	1.0	13415	9	AC079087	AC079087 Homo sapi
C 396	19	1.0	2451	14	RUBIE2	BC013788 Homo sapi	469	19	1.0	18106	9	AL450407	AL450407 Homo sapi
C 397	19	1.0	2464	10	MCANP3	BC013788 Homo sapi	470	19	1.0	18106	9	AL450407	AL450407 Homo sapi
C 398	19	1.0	2466	10	MCANP3	BC013788 Homo sapi	471	19	1.0	18106	9	AL450407	AL450407 Homo sapi
C 399	19	1.0	2570	6	CO583572	BD276297 EXTRACELL	472	19	1.0	32173	2	AC092450	AC092450 Homo sapi
C 400	19	1.0	2597	6	BD276297	BD276297 EXTRACELL	473	19	1.0	32173	2	AC092450	AC092450 Homo sapi
C 401	19	1.0	2597	6	BD276297	BD276297 EXTRACELL	474	19	1.0	32173	2	AC092450	AC092450 Homo sapi
C 402	19	1.0	2635	3	BT004849	BT004849 Drosophila	475	19	1.0	35922	9	AC145124	AC145124 Homo sapi
C 403	19	1.0	2635	3	BT004849	BT004849 Drosophila	476	19	1.0	35922	9	AC145124	AC145124 Homo sapi
C 404	19	1.0	2652	10	MMU14103	U14103 Mus muscu	477	19	1.0	36241	6	AR45366	AR45366 Sequence
C 405	19	1.0	2655	6	BD157994	BD157994 Primer fo	478	19	1.0	36241	6	AR45366	AR45366 Sequence
C 406	19	1.0	2665	6	AX879732	AX879732 Sequence	479	19	1.0	36241	6	AR45366	AR45366 Sequence
C 407	19	1.0	2665	6	AX879732	AX879732 Sequence	480	19	1.0	36241	6	AR45366	AR45366 Sequence
C 408	19	1.0	2671	6	AR075344	AR075344 Homo sapi	481	19	1.0	36241	6	AR45366	AR45366 Sequence
C 409	19	1.0	2671	6	AR075344	AR075344 Homo sapi	482	19	1.0	36241	6	AR45366	AR45366 Sequence
C 410	19	1.0	2871	5	AY228773	AY228773 Limosa ha	483	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 411	19	1.0	2871	5	AY228773	AY228773 Limosa ha	484	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 412	19	1.0	2871	5	AY228773	AY228773 Limosa ha	485	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 413	19	1.0	2871	5	AY228773	AY228773 Limosa ha	486	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 414	19	1.0	2871	5	AY228773	AY228773 Limosa ha	487	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 415	19	1.0	2871	5	AY228773	AY228773 Limosa ha	488	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 416	19	1.0	2871	5	AY228773	AY228773 Limosa ha	489	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 417	19	1.0	2871	5	AY228773	AY228773 Limosa ha	490	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 418	19	1.0	2871	5	AY228773	AY228773 Limosa ha	491	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 419	19	1.0	2871	5	AY228773	AY228773 Limosa ha	492	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 420	19	1.0	2871	5	AY228773	AY228773 Limosa ha	493	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 421	19	1.0	2871	5	AY228773	AY228773 Limosa ha	494	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 422	19	1.0	2871	5	AY228773	AY228773 Limosa ha	495	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 423	19	1.0	2871	5	AY228773	AY228773 Limosa ha	496	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 424	19	1.0	2871	5	AY228773	AY228773 Limosa ha	497	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 425	19	1.0	2871	5	AY228773	AY228773 Limosa ha	498	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 426	19	1.0	2871	5	AY228773	AY228773 Limosa ha	499	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 427	19	1.0	2871	5	AY228773	AY228773 Limosa ha	500	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 428	19	1.0	2871	5	AY228773	AY228773 Limosa ha	501	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 429	19	1.0	2871	5	AY228773	AY228773 Limosa ha	502	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 430	19	1.0	2871	5	AY228773	AY228773 Limosa ha	503	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 431	19	1.0	2871	5	AY228773	AY228773 Limosa ha	504	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 432	19	1.0	2871	5	AY228773	AY228773 Limosa ha	505	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 433	19	1.0	2871	5	AY228773	AY228773 Limosa ha	506	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 434	19	1.0	2871	5	AY228773	AY228773 Limosa ha	507	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 435	19	1.0	2871	5	AY228773	AY228773 Limosa ha	508	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 436	19	1.0	2871	5	AY228773	AY228773 Limosa ha	509	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 437	19	1.0	2871	5	AY228773	AY228773 Limosa ha	510	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 438	19	1.0	2871	5	AY228773	AY228773 Limosa ha	511	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 439	19	1.0	2871	5	AY228773	AY228773 Limosa ha	512	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 440	19	1.0	2871	5	AY228773	AY228773 Limosa ha	513	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 441	19	1.0	2871	5	AY228773	AY228773 Limosa ha	514	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 442	19	1.0	2871	5	AY228773	AY228773 Limosa ha	515	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 443	19	1.0	2871	5	AY228773	AY228773 Limosa ha	516	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 444	19	1.0	2871	5	AY228773	AY228773 Limosa ha	517	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 445	19	1.0	2871	5	AY228773	AY228773 Limosa ha	518	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 446	19	1.0	2871	5	AY228773	AY228773 Limosa ha	519	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 447	19	1.0	2871	5	AY228773	AY228773 Limosa ha	520	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 448	19	1.0	2871	5	AY228773	AY228773 Limosa ha	521	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 449	19	1.0	2871	5	AY228773	AY228773 Limosa ha	522	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 450	19	1.0	2871	5	AY228773	AY228773 Limosa ha	523	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 451	19	1.0	2871	5	AY228773	AY228773 Limosa ha	524	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 452	19	1.0	2871	5	AY228773	AY228773 Limosa ha	525	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 453	19	1.0	2871	5	AY228773	AY228773 Limosa ha	526	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 454	19	1.0	2871	5	AY228773	AY228773 Limosa ha	527	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 455	19	1.0	2871	5	AY228773	AY228773 Limosa ha	528	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 456	19	1.0	2871	5	AY228773	AY228773 Limosa ha	529	19	1.0	40397	2	AC144574	AC144574 Homo sapi
C 457	19	1.0	2871	5	AY228773	AY228773 Limosa ha	530	19	1.0	40397	2	AC144574	AC144574 Homo sapi

531	19	1.0	92697	9	AL135784	604	19	1.0	129459	10	AF372979	AP372979 Mus muscu
532	19	1.0	93717	9	AL357673	605	19	1.0	129811	9	HSB3477	AL049547 Human DNA
533	19	1.0	94027	9	AC073221	606	19	1.0	130515	10	AC117195	AC117195 Mus muscu
534	19	1.0	94595	9	AL732591	607	19	1.0	130716	10	AC140109	AC140109 Mus muscu
535	19	1.0	94766	2	AC144930	608	19	1.0	130946	10	AC129310	AC129310 Mus muscu
536	19	1.0	95850	2	AC020063	609	19	1.0	131112	9	AL157712	AL157712 Human DNA
537	19	1.0	96245	2	AC087459	610	19	1.0	131570	9	AP002495	AP002495 Homo sapi
538	19	1.0	96335	9	BSX67671	611	19	1.0	132978	2	AC097011	AC097011 Sus scrofa
539	19	1.0	97847	9	HS874C20	612	19	1.0	133337	2	AC016231	AC016231 Homo sapi
540	19	1.0	98593	9	AL356472	613	19	1.0	134267	9	AL157389	AL157389 Human DNA
541	19	1.0	99672	2	AC110531	614	19	1.0	134270	2	AC147762	AC147762 Daerypus n
542	19	1.0	99908	9	AC006464	615	19	1.0	134697	9	AC114738	AC114738 Homo sapi
543	19	1.0	100000	9	AP000079	616	19	1.0	134904	9	AC004879	AC004879 Homo sapi
544	19	1.0	100267	9	HSBHC336A	617	19	1.0	135214	9	AC004848	AC004848 Homo sapi
545	19	1.0	100538	2	AC115281_3	618	19	1.0	135321	2	AC142021	AC142021 Rattus no
546	19	1.0	103488	10	AL772395	619	19	1.0	136002	9	AC120054	AC120054 Homo sapi
547	19	1.0	104907	9	HSB3741H3	620	19	1.0	136083	4	AC091656	AC091656 Felis cat
548	19	1.0	105239	9	AL339059	621	19	1.0	136581	9	AC008459	AC008459 Homo sapi
549	19	1.0	106004	1	AP006585	622	19	1.0	137013	2	AC151827	AC151827 Mus muscu
550	19	1.0	106806	2	AF165177	623	19	1.0	137263	2	AC068740	AC068740 Homo sapi
551	19	1.0	107132	5	BSX55941	624	19	1.0	137263	2	AC068740	AC068740 Homo sapi
552	19	1.0	107413	4	AL773560	625	19	1.0	138278	9	AC137695	AC137695 Homo sapi
553	19	1.0	107532	9	AC010425	626	19	1.0	138313	9	AC092111	AC092111 Homo sapi
554	19	1.0	108873	14	AF318573	627	19	1.0	138938	2	AL928569	AL928569 Homo sapi
555	19	1.0	109039	2	AC143174	628	19	1.0	138932	9	AL662828	AL662828 Human DNA
556	19	1.0	109646	9	HSBHC8822	629	19	1.0	139126	10	AC126608	AC126608 Mus muscu
557	19	1.0	110000	2	AC092450_0	630	19	1.0	140148	9	AL354916	AL354916 Human DNA
558	19	1.0	110000	2	AC092450_6	631	19	1.0	140292	9	CNS01D08	AL133223 Human chr
559	19	1.0	110000	2	AC097542_0	632	19	1.0	141456	9	AL355300	AL355300 Human DNA
560	19	1.0	110000	2	AC097542_1	633	19	1.0	141591	9	AC079467	AC079467 Homo sapi
561	19	1.0	110000	2	AC107421_1	634	19	1.0	141674	2	AC080046	AC080046 Homo sapi
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AUTHORS	Ono, T., Kurashige, T., Harada, N., Noguchi, Y., Saika, T., Nikiwa, N., Aoe, M., Nakamura, S., Higashi, T., Hiraki, A., Wada, H., Kumon, H., Old, L. J. and Nakayama, E.
TITLE	Identification of proacrosin binding protein sp32 precursor as a human cancer/testis antigen
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3282-3287 (2001)
MELINE	21145836
PUBMED	11248070
REFERENCE	2 (Bases 1 to 1886)
AUTHORS	Ono, T. and Nakayama, E.
TITLE	Direct Submission
JOURNAL	Submitted (27-NOV-2000) Toshiro Ono, Okayama University Medical School, Department of Immunology; 2-5-1 Shikata-cho, Okayama, Okayama, 700-8558, Japan E-mail: onetomed.okayama-u.ac.jp, Tel:81-86-235-7192, Fax:81-86-235-7193
FEATURES	Location/Qualifiers
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AUTHORS			
TITLE			
JOURNAL			
REMARK			
COMMENT			

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1861 TGACTTACATAAATGTTGATCTTC 1886

1861 TGACTTACATAAATGTTGATCTTC 1886

BC033010 1899 bp mRNA linear PRI 30-JUN-2004

Homo sapiens acrosin binding protein, mRNA (cDNA clone MGC:26629 IMAGE:4822765), complete cds.

BC033010

BC033010.2 GI:34783873

MGC.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1899)

Strausberg,R.J., Fengold,E.A., Grouse,L.H., Dergs,J.G., Klausner,R.D., Collins,F.S., Wagner,K.H., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buelow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Datchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldi,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Udell,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loughellano,N.A., Peters,G.J., Abramson,R.D., Mullany,S.J., Boeck,S.A., McKean,P.J., McKernan,K.T., Malek,U.A., Gunaratne,P.H., Richards,S., Woley,K.C., Hale,S., Garcia,A.M., Gay,L.U., Hulyk,S.W., Vallalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,R.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butcherfield,Y.S., Krzywinski,M.I., Skalska,U.J., Smalins,D.E., Scherch,A., Schein,J.E., Jones,S.U., and Marz,M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 1899)

Strausberg,R.

Direct Submission

Submitted (21-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

On Sep 16, 2003 this sequence version replaced gi:21542511.

Contact: MGC help desk

Email: gcgabs-remail.nih.gov

1861 TTGGGTTTGACCAACAGTCCCAAGAGGCGCACGTTGGAGCTGCGCCCTCTTAAAGA 1866

1861 TGACTTACATAAATGTTGATCTTC 1886

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BC033010 1899 bp mRNA linear PRI 30-JUN-2004

Homo sapiens acrosin binding protein, mRNA (cDNA clone MGC:26629 IMAGE:4822765), complete cds.

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BC033010.2 GI:34783873

MGC.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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1861 TGACTTACATAAATGTTGATCTTC 1886

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AUTHORS Bandman,O., Hillman,J.L., Baughn,M.R., Azimzai,Y., Guegler,K.J.,
Corley,N.C., Yue,H., Tang,T.Y., Reddy,R., Patterson,C., Young,J.A.,
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OLGA BANDMAN,JENNIFER L HILLMAN,MARIAH R BAUGHN,YALDA AZIMZAI, PI
KARL J GUEGLER,NEIL C CORLEY,HENRY YUE,TOM Y TANG,ROOPA REDDY, PI
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DB 1037 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1096
QY 1081 GCTTGAAGTACATGAGAGAGAGATCTTGTGTTGGGAAAGTGGTCTGTGACAGCTT 1140
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 Qy 1621 GACGTGTGCTTGCATGAGAGCAGGAGTTCAGACCTTGAAGCCAGTTGCGATGA 1680
 Db 1637 GACGTGTGCTTGCATGAGAGCAGGAGTTCAGACCTTGAAGCCAGTTGCGATGA 1696
 Qy 1681 GCTGGGCTATTTCTGCGCCACACCCGAGCCCACTGCTCCATTTGTTTGAAG 1740
 Db 1697 GCTGGGCTATTTCTGCGCCACACCCGAGCCCACTGCTCCATTTGTTTGAAG 1756
 Qy 1741 ACCCATGTGCTTTCAGGCTGCTGCTTGTGGTCTGTTACTGCGCCCTTACTCACTTCC 1800
 Db 1757 ACCCATGTGCTTTCAGGCTGCTGCTTGTGGTCTGTTACTGCGCCCTTACTCACTTCC 1816
 Qy 1801 TTGGGTTGAGCAACATGCTCCACAGAGGCGCAGGTGAGAGCTGCGCTTCTTAAAGA 1860
 Db 1817 TTGGGTTGAGCAACATGCTCCACAGAGGCGCAGGTGAGAGCTGCGCTTCTTAAAGA 1876
 Qy 1861 TGACTTTACATTAATGTTGATCTTCAAAAAA 1895
 Db 1877 TGACTTTACATTAATGTTGATCTTCAAAAAA 1911

RESULT 4
 LOCUS BD192303 1899 bp DNA linear PAT 17-JUL-2003
 DEFINITION Secreted proteins and polynucleotides encoding them.
 ACCESSION BD192303
 VERSION BD192303.1 GI:33002042
 KEYWORDS JP 2002513294-A/6.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 1899)
 AUTHORS Jacobs,K., McCoy,J.M., Lavallie,E.R., Racie,L.A., Trenc,M.,
 TITLE Spaulding,V., Agostino,M.J., Howes,S.H. and Fechtel,K.,
 JOURNAL Secreted proteins and polynucleotides encoding them
 Patent: JP 2002513294-A 6 08-MAY-2002;
 GENETICS INSTITUTE INC
 COMMENT
 PN JP 2002513294-A/6
 PD 08-MAY-2002
 PF 18-JUN-1998 JP 199504681
 PR 19-JUN-1997 US 08/878715,17-JUN-1998 US 09/098568 PI
 KENNETH JACOBSON, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI
 MAURICE TRENCY
 PI VIKKI SPAULDING, MICHAEL J AGOSTINO, STEVEN H HOWES, KIM FECHTEL
 PC C07K1/00, C07H21/02, A61K39/00, C12N1/20
 CC Strandedness: Double;
 Topology: Linear;

FEATURES FH Key Location/Qualifiers.
 source 1..1899
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

Query Match 78.8%; Score 1494; DB 6; Length 1899;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1594; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GCTTGTGTCACGAGGACGCGGGGCGATCTTTTCCGCGCATGAGAAAGCAGCCGCTGCT 70
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 Qy 71 TCCCTTCCCTCAGCTCGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 130
 Db 65 TCCCTTCCCTCAGCTCGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 124
 Qy 131 GCACTAGGCGCCCACTCCAGGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 190
 Db 125 GCACTAGGCGCCCACTCCAGGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 184
 Qy 191 CACTGTGACTCCAACTGGAAGGAGAGACCTACCTGCTGCTGCTGCTGCTGCTGCTGCT 250
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 Qy 251 GCGGAAATCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 310
 Db 245 GCGGAAATCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 304
 Qy 311 GTGCTGTGCTGCTCAACTCTCTTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 370
 Db 305 GTGCTGTGCTGCTCAACTCTCTTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 364
 Qy 371 ACTACCGTGTCTCAACACAGTGTCTATATGCAAGAGAGTCTGCTGCTGCTGCTGCT 430
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 Qy 431 CTATTTCTGCACTTCACTCTCAAGGAGTGAAGCTTCAAGTGTCAAGTGTCAAGTGT 490
 Db 425 CTATTTCTGCACTTCACTCTCAAGGAGTGAAGCTTCAAGTGTCAAGTGTCAAGTGT 484
 Qy 491 CGATGACTCTCCCACTCTCAAGGAGTGAAGCTTCAAGTGTCAAGTGTCAAGTGTCAAG 550
 Db 485 CGATGACTCTCCCACTCTCAAGGAGTGAAGCTTCAAGTGTCAAGTGTCAAGTGTCAAG 544
 Qy 551 GGCCTGAGAGGCTCAAGCAAGCTGGAAGAGCTCCCTCAAGTGTCTGCTGCTGCTG 610
 Db 545 GGCCTGAGAGGCTCAAGCAAGCTGGAAGAGCTCCCTCAAGTGTCTGCTGCTGCTG 604
 Qy 611 GCCAGAGCAAGCGCGAGAGCAAGGAGCAAGGAGTGAAGCAAGGAGTGAAGCAAGGAG 670
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 Qy 851 TTGCTCTCCGAGTGAAGAGTGAAGTCTCTCTATGATGAGGAGGAGGAGGAGGAGGAG 910
 Db 845 TTGCTCTCCGAGTGAAGAGTGAAGTCTCTCTATGATGAGGAGGAGGAGGAGGAGGAG 904
 Qy 911 TCATTCGATCAGCCCAAGAAATGATGAAATGATGAAATGATGAAATGATGAAATGATCT 970

Db	905	TCATTGCATCAGCCCAAGGAATNAGTGAATGAATGAATNATATGATGAAACTCTACT	964		
QY	971	GGAGAAACCAAAACCTTGGCAGCTTCTTGCAGCTGCCCAACAGAGGCTTTGCTGTGC	1030		
Db	965	GGAGAAACCAAAACCTTGGCAGCTTCTTGCAGCTGCCCAACAGAGGCTTTGCTGTGC	1024		
QY	1031	TGTGCTATTCGATCGTGGAGAAATACATGATCATTAATCCCAACAGCCAGGCTGTGAAGT	1094		
Db	1025	TGTGCTATTCGATCGTGGAGAAATACATGATCATTAATCCCAACAGGCTGTGAAGT	1084		
QY	1091	ACATGAGAGAGAGATCCTTGGATTCCGGAAGTCGGTCTGTGACAGGCTTTGGGCGGAC	1150		
Db	1085	ACATGAGAGAGAGATCCTTGGATTCCGGAAGTCGGTCTGTGACAGGCTTTGGGCGGAC	1144		
QY	1151	ACATGCTACCTGTGCTCCTGTGTGACATTCGTCTGCTTGAAGCTGAGGACGACCTAG	1210		
Db	1145	ACATGCTACCTGTGCTCCTGTGTGACATTCGTCTGCTTGAAGCTGAGGACGACCTAG	1204		
QY	1211	AGGCGAGCTGTGAGGCGAACATATGACACCTCCCAAGAATCCTTTGTCAAGCCCT	1270		
Db	1205	AGGCGAGCTGTGAGGCGAACATATGACACCTCCCAAGAATCCTTTGTCAAGCCCT	1264		
QY	1271	TGCTTGCCTCCAGAGCGCTGTGTCATCGGCAACAGGTAGGGTCCCAATCAGGCGCT	1330		
Db	1265	TGCTTGCCTCCAGAGCGCTGTGTCATCGGCAACAGGTAGGGTCCCAATCAGGCGCT	1324		
QY	1331	TTTACGGGCTGGATTGTACGGTGGCTCAATGACCTTCTGTGTGCCCGCTTGTGCA	1390		
Db	1325	TTTACGGGCTGGATTGTACGGTGGCTCAATGACCTTCTGTGTGCCCGCTTGTGCA	1384		
QY	1391	CGAAAGGCTGTGAGATGTCCGAGTCTCTGAGTGGCTCCAGACTGAGTTCCTTAGCTTC	1450		
Db	1385	CGAAAGGCTGTGAGATGTCCGAGTCTCTGAGTGGCTCCAGACTGAGTTCCTTAGCTTC	1444		
QY	1451	AGGATGGGGATTTCCCTACCAAGATTTTGTGACACAGATATATCCAGTACCCAACTACT	1510		
Db	1445	AGGATGGGGATTTCCCTACCAAGATTTTGTGACACAGATATATCCAGTACCCAACTACT	1504		
QY	1511	GTTCCCTTCAAAAGCAGCAGTGTCTGATGAGAAAACCGCAATCGGAAGGTGCCGCAATGA	1570		
Db	1505	GTTCCCTTCAAAAGCAGCAGTGTCTGATGAGAAAACCGCAATCGGAAGGTGCCGCAATGA	1564		
QY	1571	GATGCTGTGAGATGAGACTTACAGTGGCGCTGAGCC	1606		
Db	1565	GATGCTGTGAGATGAGACTTACAGTGGCGCTGAGCC	1600		
RESULT 5	BD136402	1692 bp	DNA	linear	PAT 18-SEP-2002
LOCUS	BD136402				
DEFINITION	95 human secretory proteins.				
ACCESSION	BD136402				
VERSION	BD136402.1	GI:23231347			
KEYWORDS	JP 2002506627-A/89.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	1 (bases 1 to 1692)				
TITLE	Ruben,S.M., Ni,J., Rosen,C.A., Yu,G.L., Young,P.E., Fen,P., Soppel,D.R., Wei,Y.F., Endress,G.A., Dunn,R.D., Kyaw,H., Ebner,R., Lafleur,D.W., Olsen,H.S., Shi,Y. and Moore,P.A.				
JOURNAL	95 human secretory proteins Patent: JP 2002506627-A 89 05-MAR-2002;				
COMMENT	HUMAN GENOME SCIENCES INC OS Homo sapiens (human) PN JP 2002506627-A/89 PD 05-MAR-2002 PF 18-MAR-1999 JP 2000536733 PR 19-MAR-1998 US 60/078573,19-MAR-1998 US 60/078574 PR 19-MAR-1998 US 60/078579,19-MAR-1998 US 60/078578 PR				

[illegible]

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Db	682	GGGGCAGAAACAGAAAGACAA	GAAAGGAAACGAAAGAGGG	AAAGCAGAAAG	752		
QY	753	ACAGGGGACTAAGGAGGAGG	AGGCTGTGTCTCAGCTG	CAGACAGCTCAGGCCCA	812		
Db	742	ACAGGGGACTAAGGAGGAGG	AGGCTGTGTCTCAGCTG	CAGACAGCTCAGGCCCA	812		
QY	813	GTTCACCTGTAATCTGTAT	CTTCTAACCTTCCTTTT	CTCTCCCGGGTACGAAAGT	872		
Db	802	GTTCACCTGTAATCTGTAT	CTTCTAACCTTCCTTTT	CTCTCCCGGGTACGAAAGT	872		
QY	873	AGAGTCTACTCTATGATAT	GATGAGAAACATCCAGAG	CTCATTTGATCAGCCAGGAAT	932		
Db	862	AGAGTCTACTCTATGATAT	GATGAGAAACATCCAGAG	CTCATTTGATCAGCCAGGAAT	932		
QY	933	AGATGAAATGAAATATAT	TATGATGAAACTCTTAC	TGTGAGAAACCAAAACCTTGGCAG	992		
Db	922	AGATGAAATGAAATATAT	TATGATGAAACTCTTAC	TGTGAGAAACCAAAACCTTGGCAG	992		
QY	993	CTTCTCGACGCTGCCCA	CAGAGAGGCTTGTGTGTG	CTGTGCTATTTGATCTGTGAGAA	1052		
Db	982	CTTCTCGACGCTGCCCA	CAGAGAGGCTTGTGTGTG	CTGTGCTATTTGATCTGTGAGAA	1052		
QY	1053	TACCTGCATCATAAACCC	CAAGCAAGGCTGTGAAAT	CATGAGAGAGAGATCTTGG	1112		
Db	1041	TACCTGCATCATAAACCC	CAAGCAAGGCTGTGAAAT	CATGAGAGAGAGATCTTGG	1112		
QY	1113	TTTGGGAAAGTCGTCTGT	GTGACAGCTTGGGGGGGCA	CAATGTCTAACCTGTGCTCTG	1172		
Db	1101	TTTGGGAAAGTCGTCTGT	GTGACAGCTTGGGGGGGCA	CAATGTCTAACCTGTGCTCTG	1172		
QY	1173	TGACTTGTGCTCTTGAAG	CTGAGAGGCACTCAAGGCC	CAAGCTTGCAGGGGCAACA	1232		
Db	1161	TGACTTGTGCTCTTGAAG	CTGAGAGGCACTCAAGGCC	CAAGCTTGCAGGGGCAACA	1232		
QY	1233	ATGCGAACCTCCCA	CANAAGCTCTTTGTCA	AGCCCTTGTGCTTGCCTCCAGAGCCTGTGC	1292		
Db	1221	ATGCGAACCTCCCA	CANAAGCTCTTTGTCA	AGCCCTTGTGCTTGCCTCCAGAGCCTGTGC	1292		
QY	1293	CATCGGCAACAGAGTA	AGGATGCCCAATCAGG	CCGGCTTTTACGGGCTGATTTTGCAGG	1352		
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QY	1353	TGGGCTCCA	CATGCACTTCTGGTGG	CCGGCTTGCACGAAAGCTGTGAAGATGCCG	1412		
Db	1340	TGGGCTCCA	CATGCACTTCTGGTGG	CCGGCTTGCACGAAAGCTGTGAAGATGCCG	1412		
QY	1413	AGTCTCTGGGAGGCTCC	AGACTGATGCTTACCTT	CCAGATGAGGAAATTTCCCTACCA	1472		
Db	1400	AGTCTCTGGGAGGCTCC	AGACTGATGCTTACCTT	CCAGATGAGGAAATTTCCCTACCA	1472		
QY	1473	GATTTGTGACACAGACTA	TATTCAGATACCAAACTA	CTGTTCTTCAAAAGCCAGCAGTG	1532		
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QY	1533	TCTGATGAGAAACCGCA	ATCGAAGGTGCCGATGAG	ATGTCTGAGAAATGAGACTTA	1592		
Db	1519	TCTGATGAGAAACCGCA	ATCGAAGGTGCCGATGAG	ATGTCTGAGAAATGAGACTTA	1592		
QY	1593	CAGTGGCTGAGGCCCTG	CAAAAGTAGAGACGTTG	CTTCGATATGAGACAGAGTTCCAG	1652		
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QY	1713	ACCTGGCCACGTTCTTA	TGTTTGTGAACCCAT	TGCTTGAAGCTGCCCTTCTGGGT	1772		
Db	1699	ACCTGGCCACGTTCTTA	TGTTTGTGAACCCAT	TGCTTGAAGCTGCCCTTCTGGGT	1772		
	1758	ACCTGGCCACGTTCTTA	TGTTTGTGAACCCAT	TGCTTGAAGCTGCCCTTCTGGGT	1758		

OY	1773	CTGTTACTGGGCCCTTACTCACAATTTTCCTTGAGTGTGAACCAACAGTCCCGAAGAGGCCA	1832		
Db	1759	CTGTACTCGGCCCTTACTCACATTTCCTTGAGTGTGAACCAACAGTCCCGAAGAGGCCA	1818		
RESULT 6	CQ722423	2299 bp	DNA	linear	PAT 03-FEB-2004
LOCUS	CQ722423				
DEFINITION	Sequence 8357 from Patent WO02068579.				
ACCESSION	CQ722423				
VERSION	CQ722423.1	GI:42283280			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Euteria; Primates; Catarrhini; Hominiidae; Homo.				
TITLE	Venter, C.J., Adams, M.C., Li, P.W., and Myers, E.W. Kites, such as nucleic acid arrays, and Myers, E.W. humans or transcripts, for detecting expression and other uses thereof Patent: WO 02068579-A 8357 06-SEP-2002; PE Corporation (NY) (US) Location/Qualifiers 1..2299 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"				
JOURNAL					
FEATURES					
source					
ORIGIN					
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Matches 769; Conservative					
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Db	356	ACCTGCACACAGACTCAGAGCCCCAAAGTTTCACTGTGATCTATCTTAAACCCTTCT	415		
OY	848	CTTTTGCTCCCCGGGTAAGAGAAGTAGCTACTCTCATGATAATGAGAACATCCAG	907		
Db	416	CTTTTGCTCCCCGGGTAAGAGAAGTAGCTACTCTCATGATAATGAGAACATCCAG	475		
OY	908	AGCTCATTCGATCAGGCCAGAAATGATGAATGAATGAATATATGATGAACTCT	967		
Db	476	AGCTCATTCGATCAGGCCAGAAATGATGAATGAATGAATATATGATGAACTCT	535		
OY	968	ACTGAGAAAACCAAACCTTGAGAGTCTCTCAGCTGCCACAGAGGCTTGTCTG	1027		
Db	536	ACTGAGAAAACCAAACCTTGAGAGTCTCTCAGCTGCCACAGAGGCTTGTCTG	595		
OY	1028	TGCTGTGCTATTCGATCGTGAAGAAATCCTGATATTAACCCCAAGCCAGGCTTGA	1087		
Db	596	TGCTGTGCTATTCGATCGTGAAGAAATCCTGATATTAACCCCAAGCCAGGCTTGA	655		
OY	1088	AGTACATGAGAGAGAGATCTTGTGTTTGGGAGAGTGGTCTGTGAAGAGCTTGGCGGC	1147		
Db	656	AGTACATGAGAGAGAGATCTTGTGTTTGGGAGAGTGGTCTGTGAAGAGCTTGGCGGC	715		
OY	1148	GACACATGTCTACCTGTGCTCTGTGAATTTTGTCTCTTGAAGCTGAGAGTGCAC	1207		
Db	716	GACACATGTCTACCTGTGCTCTGTGAATTTTGTCTCTTGAAGCTGAGAGTGCAC	775		
OY	1208	CAGAGGCGAGCTGACAGCGGAAACAATGCGACCTTCCCAAGAGCTGCTTTGTCA	1267		
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OY	1268	CTTTGCTGCTCCCGAGAGCTGTCCATGAGGAAACAGGTAGGTTCCCGAATCAG	1327		
Db	836	CTTTGCTGCTCCCGAGAGCTGTCCATGAGGAAACAGGTAGGTTCCCGAATCAG	895		
OY	1328	GCTTTACGGGCGGATTTGACGTGGGCTTCCATGAGACTTGTGGGTGCTCCGGCTG	1387		

Db 896 GCTTTACGGGCTGAGATTGTGACGTGGGCTCCACATGACTTCTGTGTGTCGCCGCTTG 955
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Db 1016 TCCAGAGTGGGATTTCCCTACCAAGATTGTGACACAGACTATATCAGTACCCAACT 1075
QY 1508 ACTGTTCTTCAAAAGCCAGACTGTGTGATGAGAAACCCGATCCGAG 1557
Db 1076 ACTGTTCTTCAAAAGCCAGACTGTGTGATGAGAAACCCGATCCGAG 1125
RESULT 7
BD139445 964 bp DNA linear PAT 18-SEP-2002
LOCUS BD139445
DEFINITION Extended cDNA of secretory protein.
ACCESSION BD139445 GI:23234390
VERSION BD139445.1
KEYWORDS JP 2002508182-A/197.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Bougueleret, L., Duclet, A. and Edwards, J.B.D.M.
AUTHORS Extended cDNA of secretory protein
TITLE Patent: JP 2002508182-A 197 19-MAR-2002;
JOURNAL GENSET
COMMENT OS Homo sapiens (human)
PN JP 2002508182-A/197
PD 19-MAR-2002 JP 2000539136
PF 17-DEC-1998 US 60/069957, 09-FEB-1998 US 60/074121 PR
PR 13-APR-1998 US 60/081563, 10-AUG-1998 US 60/096116 PI LYDIE
BOUGUELERET, AYMERIC DUCLET, JEAN BAPTISTE DUMAS MILNE PI EDWARDS
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12Q1/68, C12N15/00, C12N5/00, C12N15/00 CC
Von Heijne matrix
CC score 8.5
CC seq LKVLILPLAPAA/OD
FH Key Location/Qualifiers
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Best Local Similarity 99.3%; Pred. No. 2,7e-295;
Matches 948; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
QY 30 GGGCGGATCTTCTCCGGCCATGAGAAAGCCAGCGGTGCTTCTCCCTCCATCCCGAA 89
Db 2 GGGCGGATCTTCTCCGGCCATGAGAAAGCCAGCGGTGCTTCTCCCTCCATCCCGAA 61
QY 90 GGTGCTCTCTGCTCTGTGGACCTGCGGAGCCAGAGATTGACTAGGCCCCCACTCC 149
Db 62 GGTGCTCTCTGCTCTGTGGACCTGCGGAGCCAGAGATTGACTAGGCCCTCCACTCC 121
QY 150 AGGACACCTCTCTCTCCCTACCGAATACGAAGCGTTCTTGGCACTGTGACTCCAACTG 209
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Db 182 GAAAGCAGACTACTGCTCCGCTCCGTGCAACCCAGCGCTGCCGAGATCCACACTCGT 241
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Db 242 CCACTGAGCCATATGAAAACCAAGCCTTAGAGCCGAGTGGTGTCTGCTCCAACT 301
QY 330 CCTTATGCTCTGCTGTTGAGTCTTCTGTCAGCTTCACTGACTGCTGCTCAACCA 389
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QY 390 CGTCTATGCTGCAAGAGAGTCTGTGTTCCAGCCAGTCTATTTCTGCTCACTAAC 449
Db 362 CGTCTATGCTGCAAGAGAGTCTGTGTTCCAGCCAGTCTATTTCTGCTCACTAAC 421
QY 450 TCTCAAGAGATGAAAGCTTCACTGAGTCACTCAACCAACAC-GATGACTCTCCCACT 508
Db 422 TCTCAAGAGATGAAAGCTTCACTGAGTCACTCAACCAACAC-GATGACTCTCCCACT 481
QY 509 CACCCCACTTCACTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAG 568
Db 482 CACCCCACTTCACTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAG 541
QY 569 ACAACGTGAAAGTCTCTAACAATCTCTTCTGCTGAGGAGCCAGCAAGAGCCGAG 628
Db 542 ACAACGTGAAAGTCTCTAACAATCTCTTCTGCTGAGGAGCCAGCAAGAGCCGAG 601
QY 629 AGCAACAAGCAGAGCAGAGAGTGAACACAGCAGAGCCAGCAACAACAACAAGCAG 688
Db 602 AGCAACAAGCAGAGCAGAGAGTGAACACAGCAGAGCCAGCAACAACAACAAGCAG 661
QY 689 AAGAGGGGCGAAGAACGAGAACGAGAACGAGAACGAGAACGAGAACGAGAACGAG 748
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Db 782 CCAAGTTTCACTGTAATCTCTAATCTCTTCAACCTTCTTCTGCTGCTGCTGCTGCT 841
QY 869 AGTAGAGTCTACTCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 928
Db 842 AGTAGAGTCTACTCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 901
QY 929 AATAGATGAATGATGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 983
Db 902 AATAGATGAATGATGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 956
RESULT 8
AC135892 56520 bp DNA linear PRI 25-OCT-2002
LOCUS AC135892
DEFINITION Homo sapiens 12 BAC RP11-433J6 (Rosewell) Park Cancer Institute Human
BAC Library complete sequence.
ACCESSION AC135892
VERSION AC135892.1 GI:24371346
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-ouman, F.R., Allen, C.,
Alshrocks, S.L., Amaral, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbieri, J., Benton, J., Bimonte, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowe, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Butrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhury, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,

Source

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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

unpublished.) for Human and Mouse repeatmasker (A. Smit and P. Green, Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and CDS sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

standard of double strand coverage is completed to a minimum reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities, if the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

INDIVIDUAL BASES: This sequence meets stringent quality


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QY	582 GCTCCTACATCTCTCTGTCCTGAGGAGGCAAGGCAAGGCAAGGCAAGGCAAG	641	44630	GCTCCTACATCTCTCTGTCCTGAGGAGGCAAGGCAAGGCAAGGCAAGGCAAG	44571
QY	642 GCAAGAGTGAGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG	701	44570	GCAAGAGTGAGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG	44511
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QY	882 TCTATGATATATGAGAAACATCCAGAGCTCATTCATCCAGGCAAGGCAAGG	941	44330	TCTATGATATATGAGAAACATCCAGAGCTCATTCATCCAGGCAAGGCAAGG	44271
QY	942 GAATGAATATATGATGAGAACTCTTCTCTGAGAAACCAAAACCTTGCGAG	992	44270	GAATGAATATATGATGAGAACTCTTCTCTGAGAAACCAAAACCTTGCGAG	44220

RESULT 9
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 DEFINITION Homo sapiens chromosome 12 clone RP4-761J14, RP11-433J6, ***
 ACCESSION AC079387
 VERSION AC079387.1
 KEYWORDS HTG; HTGS PHASE1.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 245880)
 Muzny, D.M., Adams, C., Bailey, M., Barabara, J., Blankenburg, K.,
 Bodota, B., Bouck, J., Bowie, S., Brooks, C., Buhay, C., Bunac, C.,
 Burdick, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,
 David, R., Delgado, O., Deshazo, D., Ding, Y., Fernandez, C., Ferraguto, D.,
 Dugan-Rocha, S., Durbin, K.J., Fernandez, R., Ganesha, J.H., Gorrell, L.L.,
 Forcum-Tansey, J., Frantz, P., Ganesh, R., Gortell, J.H., Hoggues, M.,
 Guevara, W., Harris, K., Hernandez, J., Hodgson, A., Hughes, M.,
 Holloway, C., Hosak, H., Jackson, L.E., Jackson, L., Jia, Y., Jones, M.,
 Kelly, S., Kondolewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z.,
 Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozano, R., Lu, J.,
 Lucier, R., Martin, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M.,
 Morris, S., Nash, S., Nelson, A., Nguyen, R., Nguyen, N., Nguyen, S.,
 Oweal, G., Parish, B., Paxton, S., Payton, B., Perez, L., Pu, L.L.,
 Ouellet, M., Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S.,
 Shah, B., Shen, H., Simon, M., Sparks, A., Stamps, A., Sugeng, R.,
 Taber, P., Taylor, T., Vasquez, L., Vinson, R., Vo, Q., Wahbah, M.,
 Wellington, S., Weinstein, G., Weinstein, I.R., Williamson, A.,
 Worley, K., Wren, J., Wrensford, G., Yu, W., Zhou, X., Nelson, D. and
 Gibbs, R.

Direct Submission
 Unpublished
 2 (bases 1 to 245880)
 Worley, K.C.
 Direct Submission
 Submitted (01-SEP-2000) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On or before Sep 1, 2000 this sequence version replaced gi:4589937,
 gi:4926836, gi:4589938.

Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu

Project Information
 Center project name: J-31
 Center clone name: RP4-761J14, RP11-433J6

Summary Statistics
 Sequencing vector: M13; L08821
 Chemistry: Dye-terminator Big Dye; 92% of reads
 Chemistry: Dye-terminator Big Dye; 7% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 214565 bases at least Q40
 Consensus quality: 230283 bases at least Q30
 Consensus quality: 240000 bases at least Q20
 Estimated insert size: 29807; agarose-1p estimation
 Quality coverage: 0x in Q20 bases; agarose-1p estimation

NOTE: Estimated insert size may differ from sequence length.
 (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 NOTE: This is a "working draft" sequence. It currently
 consists of 42 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 27068: contig of 27068 bp in length
 * 27069 27168: gap of unknown length

FEATURES	source
*	240851 240950: gap of unknown length
*	240951 242140: contig of 1190 bp in length
*	242141 242240: gap of unknown length
*	242241 243504: contig of 1264 bp in length
*	243505 243604: gap of unknown length
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Ddb

65532 GCACGAGTGTGGACA CCGCAGGACC GACACAGAACCAAGCCGCACGA 701

702 ACAGAAAGACAAAGAGCAA CAGGAGAGGAGGAGCTATGATGATGCTATTCCTGTTG TTT

Oxy

[illegible][illegible]

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942 GAATGAAATATATGATGAGAACTCCTACTGGAAACCAAAACCCTGGCAG 992
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65332 GAATGAATATATGATGAGAACTCCTACTGGAAACCAAAACCCTGGCAG 65289
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RESULT 10
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OCUS
HUNYP42A04
516 bp
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11

Accession	Gene	Accession	Gene	Accession	Gene
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U00098	5S rRNA	U00098	5S rRNA	U00098	5S rRNA
U00099	16S rRNA	U00099	16S rRNA	U00099	16S rRNA
U00100	23S rRNA	U00100	23S rRNA	U00100	23S rRNA
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ORGANISM	Genus	Family
Homo sapiens	Homo	Hominidae
Eukaryota; Metazoa;		
Mammalia; Eutelesia;		
Primates; Catarrhini; Hominoidea; Homo.		
1 (bases 1 to 516)		

MOSSMANS, J., Tan, F., Maria, M., Kucaba, T., Yaddell, M., Martin, J.,
Marth, G., Bowles, L., Wylie, T., Bowers, Y., Steptoe, M., Thaising, B.,
Geisel, S., Allen, M., Underwood, K., Chappell, J., Persson, B.,
Gibbons, M., Harvey, N., Pape, D., Chamberlain, A., Morales, R.,
Schurr, D.

TITLE	Author(s)
Full Clone Sequencing of the Longest Available Member from Each	Wilson, R. and Waterston, R.

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Unigene Cluster
Unpublished
2 (bases 1 to 516)
Waterston, R.
Direct Submission
Submitted (24-AUG-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
SUBMITTED BY:
Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:est@watson.wustl.edu

COMMENT

NOTICE: This sequence represents the full insert of this cDNA. No attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted separately.

SIMILARITY INFORMATION:
similar to Sus scrofa domestica protein A54424 (PID:g1082952)
acrosomal protein sp32 precursor - pig (fragment)

FEATURES

The location of this clone is unknown.

Location/Qualifiers

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ORIGIN

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Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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417 TTCTCTGGTTGAGCAACAGTCCCAAGAGGCGCAGTGGAGAGTGCGCCCTCTTAA 476

QY 1857 AAGATGACTTTACATAAATGTTGATCTTCAAAAAA 1895
DB 477 AAGATGACTTTACATAAATGTTGATCTTCAAAAAA 515

RESULT 11
BD060281 308 bp DNA linear PAT 27-AUG-2002

LOCUS BD060281
Secreted expressed sequence tags (ESTs).

ACCESSION BD060281
BD060281.1 GI:22605887

VERSION JP 2001518793-A/641.

KEYWORDS Zea mays

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

AUTHORS 1 (bases 1 to 308)
Treacy, M., McCoy, J.M., Lavallie, E.R., Racine, L.A., Werberg, D.,

TITLE Secreted expressed sequence tags (ESTs)

JOURNAL Patent: JP 2001518793-A 641 16-OCT-2001;

GENETICS INSTITUTE INC

PN JP 2001518793-A/641

PD 16-OCT-2001

PR 10-APR-1997 US 08/837312

PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACINE, PI DAVID MERBERG,

PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC

C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC

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Key Location/Qualifiers

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ORIGIN

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Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 414 GTGTCCCAAGCCAGTCTTATTTCTTCACCTTAACCTTCAAGAGATAGACTTCAGC 473
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DB 82 TGAAGTCTACCCCAACCAAGATGACCTTCCCATCTCAACCCCACTTCAAGTGAAGAAG 141
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DB 142 CCAAGCTTCCAGCCCTGAGCTGAGAGGCTCAAGCAACAAGTGAAGCTCTTCAATC 201
QY 594 CTCCTTGTCTTGGAGGCGCAGAGCAAGGCCAGACCAAGCAGAGCAGAGAGTGA 653
DB 202 CTCCTTGTCTTGGAGGCGCAGAGCAAGGCCAGACCAAGCAGAGCAGAGAGTGA 261
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DB 262 GCACAGGCAAGAGCCGACACAAACAACAAGCAGAGAGG 302

RESULT 12

LOCUS BD179252

DEFINITION Cancer associated gene.

ACCESSION BD179252

VERSION BD179252.1 GI:30016521

BD179252 507 bp DNA linear PAT 16-APR-2003

KEYWORDS WO 02083899-A/230.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Yoshioka, Y., Okamoto, S., Oura, T., Junichi, Mineno, Asada, K., Kato, I., Inoue, H. and Mori, M.
TITLE Cancer associated gene
JOURNAL Patent: WO 02083899-A 230 24-OCT-2002; TAKARA SHUZO CO LTD, YOSHIE YOSHIKAWA, SACHIKO OKAMOTO, TOMONORI OURA, JUNICHI MINENO, KIYOZO ASADA, IKUNOSHIN KATO, HIROSHI INOUE, MASAKI MORI

COMMENT OS Homo sapiens (human)
PN WO 02083899-A/230
PD 24-OCT-2002
PF 28-MAR-2002 WO 2002JP003038
PR 10-APR-2001 JP 01P 112039, 21-SEP-2001 JP 01P 290193 PI
YOSHIE YOSHIKAWA, SACHIKO OKAMOTO, TOMONORI OURA, JUNICHI PI
MINENO, KIYOZO ASADA,
PI IKUNOSHIN KATO, HIROSHI INOUE, MASAKI MORI
PC C12N15/12, C07K14/82, C07K16/32, C12P21/08, C12Q1/68, A61K39/395,
PC A61K48/00,
PC A61P35/00, G01N33/50, G01N33/53
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FH Key
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FEATURES
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QY 1676 GATGAGCTGGCGTCTATTCTGCCCAACCCAGCCCAACCTGCCCAAGCTTCTATTGTT 1735
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Db 476 AAAAGATGACTTTACATAAATGTTGATCTTC 506

RESULT 13
BD179034
LOCUS BD179034 522 bp DNA linear PAT 16-APR-2003
DEFINITION Cancer associated gene.
ACCESSION BD179034
VERSION BD179034.1 GI:30016302
KEYWORDS WO 02083899-A/12.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Yoshioka, Y., Okamoto, S., Oura, T., Junichi, Mineno, Asada, K., Kato, I., Inoue, H. and Mori, M.
TITLE Cancer associated gene
JOURNAL Patent: WO 02083899-A 12 24-OCT-2002; TAKARA SHUZO CO LTD, YOSHIE YOSHIKAWA, SACHIKO OKAMOTO, TOMONORI OURA, JUNICHI MINENO, KIYOZO ASADA, IKUNOSHIN KATO, HIROSHI INOUE, MASAKI MORI

COMMENT OS Homo sapiens (human)
PN WO 02083899-A/12
PD 24-OCT-2002
PF 28-MAR-2002 WO 2002JP003038
PR 10-APR-2001 JP 01P 112039, 21-SEP-2001 JP 01P 290193 PI
YOSHIE YOSHIKAWA, SACHIKO OKAMOTO, TOMONORI OURA, JUNICHI PI
MINENO, KIYOZO ASADA,
PI IKUNOSHIN KATO, HIROSHI INOUE, MASAKI MORI
PC C12N15/12, C07K14/82, C07K16/32, C12P21/08, C12Q1/68, A61K39/395,
PC A61K48/00,
PC A61P35/00, G01N33/50, G01N33/53
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176 AGGTGTCCCGATGATGATGCTGCAAGATGAGACTTAAAGTGGCTGAGCCCTGGCAAAA 235
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QY 1736 TTGAGACCCCAATGCTTCAAGCGTCCCTTCTGGGTCTGTACTGCGGCCCTACTCACA 1795
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QY 1796 TTTCCTTGGGTGGAGCAACAGTCCAGAGAGGCGCAAGTGGAGCTCGCCCTCTCTTA 1855
Db 416 TTTCCTTGGGTGGAGCAACAGTCCAGAGAGGCGCAAGTGGAGCTCGCCCTCTCTTA 475
QY 1856 AAAAGATGACTTTACATAAATGTTGATCTTC 1886
Db 476 AAAAGATGACTTTACATAAATGTTGATCTTC 506

RESULT 14
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DEFINITION human STS WI-30262, sequence tagged site.
ACCESSION G23540
VERSION G23540.1 GI:1343866
KEYWORDS STS; STS sequence, primer; sequence tagged site.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 391)

AUTHORS Hudson,T.
TITLE Whitehead Institute/MIT Center for Genome Research; Physically
JOURNAL Mapped STS
COMMENT Unpublished (1995)

Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: AGTCATCTTTAAGAGGCGG
Primer B: AGACCCATTGCTTCAGC
STS size: 126
PCR profile:

Presoak:
Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35

Thermal Cycler:

Protocol:
Template: 10 ng
Primer: each 5 pm
dNTPs: each 4 mM
Tag Polymerase: 0.025 units/ul
Total Vol: 20 ul

Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 9.3

FEATURES
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DB 186 CACCCAGGCCCACTGCGCCAGTTCCTATTGTTTGAGACCCCATGCTTCAGGCTG 127
QY 1761 CCCCTTCTGGGCTGTACTCGGCCCTTACTCATTCTCTGGGTTGAGACAAGTCC 1820
DB 126 CCCCTTCTGGGCTGTACTCGGCCCTTACTCATTCTCTGGGTTGAGACAAGTCC 67
QY 1821 CAGAGAGGCCCACTGCGGGA 1840
DB 66 CAGAGAGGCCCACTGCGGGA 47

RESULT 15
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DEFINITION Sequence 60 from Patent EP1378571.

ACCESSION AX968632
VERSION AX968632.1 GI:40975063
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Lacroix,B.
TITLE 5' ESTs for secreted proteins expressed in various tissues
JOURNAL Patent: EP 1378571-A 60 07-JUN-2004;
GENSET (FR)

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ORIGIN

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DB 2 GGGCGATCTTCCGGCATGAGAGCGCGCTGCTCCTTCCCTCAGCTGAA 61
QY 90 GGTCTGCTCTGCTCTGCGACCTGCGGAGCCAGATTGACTGAGGCC 141
DB 62 GGTCTGCTCTGCTCTGCGACCTGCGGAGCCAGATTGACTGAGGCC 113

Search completed: March 8, 2005, 01:39:08
Job time: 8330 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2005, 01:39:12 ; Search time 2067 Seconds
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5401638 seqs, 2966923429 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	1886	99.5	1886	US-10-262-666-41	Sequence 41, Appl
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4	1632	86.1	1632	US-10-085-117-53	Sequence 53, Appl
5	1530	80.7	1892	US-10-719-993-124	Sequence 124, Appl
6	1494	78.8	1899	US-09-746-783-77	Sequence 77, Appl
7	1284	67.8	1892	US-09-397-945-90	Sequence 90, Appl
8	1284	67.8	1892	US-10-653-595-90	Sequence 90, Appl
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43	23	1.2	25	US-10-719-900-912511	Sequence 912511, A
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US-10-262-666-41
; Sequence 41, Application US/10262666
; Publication No. US20030180298A1
; GENERAL INFORMATION:
; APPLICANT: Nakayama, Eiichi
; APPLICANT: Ono, Toshio
; APPLICANT: Old, Lloyd J.
; APPLICANT: Hasegawa, Kosei
; APPLICANT: Matsushita, Hirokazu
; TITLE OF INVENTION: CANCER-TESTIS ANTIGENS
; FILE REFERENCE: L00461.70140
; CURRENT APPLICATION NUMBER: US/10/262,666
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: PCT/US02/12497

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; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/356,937
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/285,343
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 1886
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (49)..(1680)
; OTHER INFORMATION:
US-10-262-666-41

Query Match 99.5%; Score 1886; DB 16; Length 1886;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 3
 US-10-085-117-53
 / Sequence 53, Application US/10085117
 / Publication No. US20030232334A1
 / GENERAL INFORMATION:
 / APPLICANT: Morris, David W.
 / APPLICANT: Engelhard, Eric K.
 / TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
 / FILE REFERENCE: 529452000121
 / CURRENT APPLICATION NUMBER: US/10/085.117
 / PRIOR FILING DATE: 2002-02-27
 / PRIOR APPLICATION NUMBER: US 09/798,586
 / NUMBER OF SEQ ID NOS: 361
 / SOFTWARE: PasteSeq for Windows Version 4.0
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 / TYPE: DNA
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 US-10-085-117-53

Query Match 99.5%; Score 1886; DB 17; Length 1886;
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 QY 601 TTCCAG 660
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QY	661	PAGAGCGCGACACAAGAACACAGAGGAAGGGGCGAAACAGAAAGCGCAAGAG	720
Db	661	CAGAGCGCGACACAAGAACACAGAGGAAGGGGCGAAACAGAAAGCGCAAGAG	720
QY	721	GAAACAGAAAGAGAGGGAAGACAGGAACAGAGGACTTAAAGAGGAGCGGAGGCT	780
Db	721	GAAACAGAAAGAGAGGGAAGACAGGAAGAGAGGAGCTTAAAGAGGAGCGGAGGCT	780
QY	781	GTGTCTCAGCTGCGACAGACTCAGAGCCCAAGTTTCACTGTGAATCTCTATCTTAAAC	840
Db	781	GTGTCTCAGCTGCGACAGACTCAGAGCCCAAGTTTCACTGTGAATCTCTATCTTAAAC	840
QY	841	CCCTTCCTTTTGTGCTCCCCGGGGTACGAAAGTAGTGTACTTCTCTATGATAATGGAAGAC	900
Db	841	CCCTTCCTTTTGTGCTCCCCGGGGTACGAAAGTAGTGTACTTCTCTATGATAATGGAAGAC	900
QY	901	ATCCAGAGAGCTCATTCGATTCAGCCCGAGGAATAAGATGAAATGAAATGAAATATATATAG	960
Db	901	ATCCAGAGAGCTCATTCGATTCAGCCCGAGGAATAAGATGAAATGAAATGAAATATATATAG	960
QY	961	AACTCTTACTGAGAAACCAAAACCCTGGCAGCTTTCCTGACGTGCCCAACAGAGGCC	1020
Db	961	AACTCTTACTGAGAAACCAAAACCCTGGCAGCTTTCCTGACGTGCCCAACAGAGGCC	1020
QY	1021	TTTGCTGAGTGTGTGCTATTCGATCGTGGAATACCTGATCATATACCCCAACGCGAAG	1080
Db	1021	TTTGCTGAGTGTGTGCTATTCGATCGTGGAATACCTGATCATATACCCCAACGCGAAG	1080
QY	1081	GCCTGGAAGTACATGAGAGAGAGATCCGTGGTTTCGGGAAAGTGGGTCTGTGAACGCTT	1140
Db	1081	GCCTGGAAGTACATGAGAGAGAGATCCGTGGTTTCGGGAAAGTGGGTCTGTGAACGCTT	1140
QY	1141	GGGCGGCGACACATGTCTTACCTGTGACCCTGTGTGACTTCTGCTCCTTGAAGCTGGAGCAG	1200
Db	1141	GGGCGGCGACACATGTCTTACCTGTGACCCTGTGTGACTTCTGCTCCTTGAAGCTGGAGCAG	1200
QY	1201	TGCGCATTCAGAGGCCAGCCTCGAGCGGCAACATATGCGACACCTCCACACAGACTCCCTTT	1260
Db	1201	TGCGCATTCAGAGGCCAGCCTCGAGCGGCAACATATGCGACACCTCCACACAGACTCCCTTT	1260
QY	1261	GTCAGGCCCTTGCTGCTGCTCCGACAGCGCTGTCACATCGGCAACGAGTAGGGTCCCGCAAA	1320
Db	1261	GTCAGGCCCTTGCTGCTGCTCCGACAGCGCTGTCACATCGGCAACGAGTAGGGTCCCGCAAA	1320
QY	1321	TCAGGCGGCTTTTACGCGCTGATTTTGTACGCTGGGCTCCACATATGACTTCTGTGCTGTCC	1380
Db	1321	TCAGGCGGCTTTTACGCGCTGATTTTGTACGCTGGGCTCCACATATGACTTCTGTGCTGTCC	1380
QY	1381	CGGCTTTCGACGAAAGGCTGTGAAGATGTCCGAGTCTTGTGGGTGGCTTCAGACTGAGTTTC	1440
Db	1381	CGGCTTTCGACGAAAGGCTGTGAAGATGTCCGAGTCTTGTGGGTGGCTTCAGACTGAGTTTC	1440
QY	1441	CTTAGCTTCCAGGATAGGGGATTTTCCCTACCAAGATTGTGACACAGACTATATCCAGTAC	1500
Db	1441	CTTAGCTTCCAGGATAGGGGATTTTCCCTACCAAGATTGTGACACAGACTATATCCAGTAC	1500
QY	1501	CCAAACTACTTTCCTTCAAAAAGCCAGCAGGTGTGATGAGAGAAACCGCAATCGGAAGGTTG	1560
Db	1501	CCAAACTACTTTCCTTCAAAAAGCCAGCAGGTGTGATGAGAGAAACCGCAATCGGAAGGTTG	1560
QY	1561	TCCCGCATGAGATGTCTGCAAGATGAGCTTACAGATGAGGCTGAGCCCTGGCAAAAGTAG	1620
Db	1561	TCCCGCATGAGATGTCTGCAAGATGAGCTTACAGATGAGGCTGAGCCCTGGCAAAAGTAG	1620
QY	1621	GACGTTGTGCTTCGATGGAAGCCAGAGATTCAAGACCTTGAAGCTTCAAGGCGAGTTGGAGTA	1680
Db	1621	GACGTTGTGCTTCGATGGAAGCCAGAGATTCAAGACCTTGAAGCTTCAAGGCGAGTTGGAGTA	1680
QY	1681	GCTGGCGCTATTTCTGCCACACCCGAGCCCAACTGTGCCACGTTCTATATGTTTGTAG	1740
Db	1681	GCTGGCGCTATTTCTGCCACACCCGAGCCCAACTGTGCCACGTTCTATATGTTTGTAG	1740
QY	1741	ACCCCAATTGCTTTCAGGCGCCCTTCTGGGTCTGTATCTCGGCCCTTACTACATTCCTC	1800

Db	1741	ACCCCATTTGCTTTAAGGCTGCCCCCTTTGGGTCGTGTACTGAGCCCTTACTACATTTTC	1800
Qy	1801	TTGGGTTGGAGCAACAGTCCCGAGAGAGGCGCAGGTGGAGCTGCGCCCTCTTAAAAGA	1860
Db	1801	TTGGGTTGGAGCAACAGTCCCGAGAGAGGCGCAGGTGGAGCTGCGCCCTCTTAAAAGA	1860
Qy	1861	TGACTTTACATPAAATGTTGATCTTC	1886
Db	1861	TGACTTTACATPAAATGTTGATCTTC	1886

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RESULT 4
US-10-085-117-54
: Sequence 54, Application US/10085117
: Publication No. US20030232934A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND
FILE REFERENCE: 529452000121
CURRENT APPLICATION NUMBER: US/10/085,117
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 361
SOFTWARE: PictSeq for Windows Version 4.0.
SEQ ID NO 54
LENGTH: 1632
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-117-54

```

Query Match	86.1%;	Score 1632;	DB 17;	Length 1632;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1632;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	49	ATGAGGAAGCAGCGCTGCGCTTCTTCCCTCACTCCGAAAGTGCTGCTCGCTCTG	108
Db	1	ATGAGGAAGCAGCGCGCTGCGCTTCTTCCCTCACTCCGAAAGTGCTGCTCGCTCTG	60
Qy	109	GCACCTGCGCAGGCCAGAGATTCCAGCTAGGCCCCCACTCCAGCGACGCTCTCTCTCT	168
Db	61	GCACCTGCGCGAGGCCAGAGATTCCAGCTAGGCCCCCACTCCAGCGACGCTCTCTCTCT	120
Qy	169	ACCGAATACGAACGGCTCTTCGCACTGTGCTCACTCCAACTGGAAGCAGAGACTACCTGC	228
Db	121	ACCGAATACGAACGGCTCTTCGCACTGTGCTCACTCCAACTGGAAGCAGAGACTACCTGC	180
Qy	229	CGTCTCCGTGCAACCCACGAGCTGCCGGAATCCACACTGTGCAGCTGAGCAATATGAA	288
Db	181	CGTCTCCGTGCAACCCACGAGCTGCCGGAATCCACACTGTGCAGCTGAGCAATATGAA	240
Qy	289	AACCAAGGCTTAGTGGCCGATGAGTGTCTGTCTCCAACTCCCTTATATGCTCCGCTT	348
Db	241	AACCAAGGCTTAGTGGCCGATGAGTGTCTGTCTCCAACTCCCTTATATGCTCCGCTT	300
Qy	349	GAGTCTTCTGCGCAGTTCACTCACTACCGTTGCTCCAAACAAGTCTATATGCAAGAGA	408
Db	301	GAGTCTTCTGCGCAGTTCACTCACTACCGTTGCTCCAAACAAGTCTATATGCAAGAGA	360
Qy	409	GTCTGTGTTCCAGCGCACTCTATTTCTTCACCTTAACACTGTAAAGGATTAAGAAGT	468
Db	361	GTCTGTGTTCCAGCGCACTCTATTTCTTCACCTTAACACTGTAAAGGATTAAGAAGT	420
Qy	469	TCACTGAAGTCTCAACCCACCAAGATGACTTCCCCATCTCAACCCCACTTCAAGTGACA	528
Db	421	TCACTGAAGTCTCAACCCACCAAGATGACTTCCCCATCTCAACCCCACTTCAAGTGACA	480
Qy	529	GAAAGCCAGACTTCCAGGCGCTGCGCTGAGAGGCTCAACAACAAGTGAAGAAGCTCTTA	588
Db	481	GAAAGCCAGACTTCCAGGCGCTGCGCTGAGAGGCTCAACAACAAGTGAAGAAGCTCTTA	540

QY 589 CAATCTCTCTTGTCCCTGGAGGCGAGAGCAAGCCGACAGACAGAGAGAGAGAG 648
DB 541 CAATCTCTCTTGTCCCTGGAGGCGAGAGCAAGCCGACAGAGCAAGAGAGAGAG 600
QY 649 GTGAGGCAAGGCGAGAGGCGAGACAGAGACAGAGAGAGAGAGAGAGAGAGAG 708
DB 601 GTGAGGCAAGGCGAGAGGCGAGACAGAGACAGAGAGAGAGAGAGAGAGAGAG 660
QY 709 GAGCAAG 768
DB 661 GAGCAAG 720
QY 769 GAGAGGAG 828
DB 721 GAGAGGAG 888
QY 829 CTATCTCTTAAACCTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 888
DB 781 CTATCTCTTAAACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
QY 889 ATATATGAGAGATCATCAGAGAGCTCTATGATCAGAGAGAGAGAGAGAGAGAG 948
DB 841 ATATATGAGAGATCATCAGAGAGCTCTATGATCAGAGAGAGAGAGAGAGAGAG 900
QY 949 ATATATGAGAGATCATCAGAGAGCTCTATGATCAGAGAGAGAGAGAGAGAGAG 1008
DB 901 ATATATGAGAGATCATCAGAGAGCTCTATGATCAGAGAGAGAGAGAGAGAGAG 960
QY 1009 CACACAGAGAGCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1068
DB 961 CACACAGAGAGCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1020
QY 1069 CCCACAGAGAGCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1128
DB 1021 CCCACAGAGAGCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1080
QY 1129 TGTGACAGAGCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1188
DB 1081 TGTGACAGAGCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1140
QY 1189 AAGCTGAGAGAGCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1248
DB 1141 AAGCTGAGAGAGCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1200
QY 1249 AAGACTCTCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1308
DB 1201 AAGACTCTCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1260
QY 1309 GGGTCCCGAGAGATCAGAGAGCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1368
DB 1261 GGGTCCCGAGAGATCAGAGAGCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1320
QY 1369 TTTCTGTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1428
DB 1321 TTTCTGTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1380
QY 1429 CAGACTGAGTTCCTTACTCTTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1488
DB 1381 CAGACTGAGTTCCTTACTCTTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1440
QY 1489 TATATCTAGTACCCAACTACTGTCTCTCAAAAGCCGAGCTGTCTGTCTGTCTGT 1548
DB 1441 TATATCTAGTACCCAACTACTGTCTCTCAAAAGCCGAGCTGTCTGTCTGTCTGT 1500
QY 1549 AATCGAGAGAGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1608
DB 1501 AATCGAGAGAGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1560
QY 1609 GGCAG 1668
DB 1561 GGCAG 1620
QY 1669 CAGTTCCGATGA 1680

DB 1621 CAGTTCCGATGA 1632

RESULT 5
US-10-719-993-124
Sequence 124, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: C1001496
CURRENT APPLICATION NUMBER: US/10/719, 993
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 124
LENGTH: 1892
TYPE: DNA
ORGANISM: Homo sapiens
US-10-719-993-124

Query Match 80.7%; Score 1530; DB 18; Length 1892;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1880; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GTTAGAGCGGCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 60
DB 4 GTTAGAGCGGCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 63
QY 61 GCGCTGCTTCT 120
DB 64 GCGCTGCTTCT 123
QY 121 GCCAGAGATTCAGTCAAG 180
DB 124 GCCAGAGATTCAGTCAAG 183
QY 181 CGCTTCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 240
DB 184 CGCTTCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 243
QY 241 ACCAGAGGCTGCGGAGATTCAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 244 ACCAGAGGCTGCGGAGATTCAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
QY 301 GTGCGGAGATTCAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 304 GTGCGGAGATTCAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 363
QY 361 CAGTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 420
DB 364 CAGTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 423
QY 421 CAGGAGTCTCTATCTTCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACT 480
DB 424 CAGGAGTCTCTATCTTCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACT 483
QY 481 TCACCCAGCAGATGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
DB 484 TCACCCAGCAGATGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 543
QY 541 TTCAGGCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 600
DB 544 TTCAGGCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 603
QY 601 TTCCTGGAG 660
DB 604 TTCCTGGAG 663
QY 661 CAGAGCGGAG 720


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Db      125  GAACTCAGGCTCCAGCTCAGAGAGCCCTCTCTCTCTCCGAAATACGAGCCTTCTTGG 184
Qy      191  CACTGCTGATCTCCAACTTGGAGGAGAGAGTCACTGCGGTCTCCGTCGACACCCAGCCT 250
Db      185  CACTGCTGATCTCCAACTTGGAGGAGAGAGTCACTGCGGTCTCCGTCGACACCCAGCCT 244
Qy      251  GCCGGAATCCCACTGCTGAGCTGAGCAATATGAAACCAAGGCTTAACTGCGCGATG 310
Db      245  GCCGGAATCCCACTGCTGAGCTGAGCAATATGAAACCAAGGCTTAACTGCGCGATG 304
Qy      311  GTGCTGCTGCTCCAACTTCCCTTAATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 370
Db      305  GTGCTGCTGCTCCAACTTCCCTTAATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 364
Qy      371  ACTACGCTGCTCCAACTTCCCTTAATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 430
Db      365  ACTACGCTGCTCCAACTTCCCTTAATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 424
Qy      431  CTATTCCTGCTCACTCACTCTCTCAAGAGATGAAAGCTTGAAGCTTGAAGCTTGAAGCTT 490
Db      425  CTATTCCTGCTCACTCACTCTCTCAAGAGATGAAAGCTTGAAGCTTGAAGCTTGAAGCTT 484
Qy      491  CGATGACCTTCCCTCCATCTCACTCAAGAGATGAAAGCTTGAAGCTTGAAGCTTGAAGCTT 550
Db      485  CGATGACCTTCCCTCCATCTCACTCAAGAGATGAAAGCTTGAAGCTTGAAGCTTGAAGCTT 544
Qy      551  GGCCCTGAGAGGCTCAGAGCAAGCTGGAAGAGCTTCTTAATCTCTTCTGCTGCTGAGAG 610
Db      545  GGCCCTGAGAGGCTCAGAGCAAGCTGGAAGAGCTTCTTAATCTCTTCTGCTGCTGAGAG 604
Qy      611  GCCAGAGCAAGGCTCAGAGCAAGCTGGAAGAGCTTCTTAATCTCTTCTGCTGCTGAGAG 670
Db      605  GCCAGAGCAAGGCTCAGAGCAAGCTGGAAGAGCTTCTTAATCTCTTCTGCTGCTGAGAG 664
Qy      671  CACAAGAACCAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 730
Db      665  CACAAGAACCAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 724
Qy      731  AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 790
Db      725  AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 784
Qy      791  TGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 850
Db      785  TGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 844
Qy      851  TTGCTTCCCGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 910
Db      845  TTGCTTCCCGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 904
Qy      911  TCATTCGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 970
Db      905  TCATTCGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 964
Qy      971  GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1030
Db      965  GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1024
Qy      1031  TTGCTTCCCGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1090
Db      1025  TTGCTTCCCGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1084
Qy      1091  ACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1150
Db      1085  ACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1144
Qy      1151  ACATGCTTCACTGCTGCTCTGAGCTTCTGAGCTTCTGAGCTTCTGAGCTTCTGAGCTT 1210
Db      1145  ACATGCTTCACTGCTGCTCTGAGCTTCTGAGCTTCTGAGCTTCTGAGCTTCTGAGCTT 1204
Qy      1211  AGGCGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1270
Db      1205  AGGCGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1264

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Qy      1271  TGCTTGCTCCAGAGAGCTTCCATGCGGCAACAGAGTAGAGTCCCAAGATAGAGCCCT 1330
Db      1265  TGCTTGCTCCAGAGAGCTTCCATGCGGCAACAGAGTAGAGTCCCAAGATAGAGCCCT 1324
Qy      1331  TTTCAGGCTGAGATTTGATGAGTGGGCTCCAGATGAGATTTGAGTGGGCTTGGCA 1390
Db      1325  TTTCAGGCTGAGATTTGATGAGTGGGCTCCAGATGAGATTTGAGTGGGCTTGGCA 1384
Qy      1391  CGAAGGCTGAGATTTGATGAGTGGGCTCCAGATGAGATTTGAGTGGGCTTGGCA 1450
Db      1385  CGAAGGCTGAGATTTGATGAGTGGGCTCCAGATGAGATTTGAGTGGGCTTGGCA 1444
Qy      1451  AGATGAGGATTTGATGAGTGGGCTCCAGATGAGATTTGAGTGGGCTTGGCA 1510
Db      1445  AGATGAGGATTTGATGAGTGGGCTCCAGATGAGATTTGAGTGGGCTTGGCA 1504
Qy      1511  GTTCTTCAAAAGGCAAGAGTGTGATGAGAAACCGCAATCGAAGTGTCCGCAATGA 1570
Db      1505  GTTCTTCAAAAGGCAAGAGTGTGATGAGAAACCGCAATCGAAGTGTCCGCAATGA 1564
Qy      1571  GATGCTGAGATGAGATTTAAGTGGCTGAGCC 1606
Db      1565  GATGCTGAGATGAGATTTAAGTGGCTGAGCC 1600

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RESULT 7
US-09-397-945-90
/ Sequence 90, Application US/09397945
/ Publication No. US20030065139A1
/ GENERAL INFORMATION:
/ APPLICANT: Human Genome Sciences, Inc. et al.
/ TITLE OF INVENTION: 95 Human secreted proteins
/ FILE REFERENCE: P2027P1
/ CURRENT FILING DATE: 1999-09-17
/ PRIOR FILING DATE: 1999-09-17
/ PRIOR APPLICATION NUMBER: PCT/US99/05804
/ PRIOR FILING DATE: 1999-03-18
/ PRIOR APPLICATION NUMBER: 60/078,566
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078,576
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078,573
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078,574
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078,579
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/080,314
/ PRIOR FILING DATE: 1998-04-01
/ PRIOR APPLICATION NUMBER: 60/080,312
/ PRIOR FILING DATE: 1998-04-01
/ PRIOR APPLICATION NUMBER: 60/078,578
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078,581
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078,577
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078,563
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/080,313
/ PRIOR FILING DATE: 1998-04-01
/ NUMBER OF SEQ ID NOS: 470
/ SOFTWARE: Patent Ver. 2.0
/ SEQ ID NO 90
/ LENGTH: 1892
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-397-945-90

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Query Match      67.8%; Score 1284; DB 10; Length 1892;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1794; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

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QY 33 CGGATCTTCCGCGCATGAGAGAGCCAGCGCTGAGCTTCTTCTCACTCTGAAAGT 92
DB 22 CGGATCTTCCGCGCATGAGAGAGCCAGCGCTGAGCTTCTTCTTCTTCTCACTCTGAAAGT 81
QY 93 GCTGCTCTGCTCTGCTGAGAGAGCCAGCGCTGAGCTTCTTCTCACTCTGAAAGT 152
DB 82 GCTGCTCTGCTCTGCTGAGAGAGCCAGCGCTGAGCTTCTTCTTCTTCTCACTCTGAAAGT 141
QY 153 CAGCGCTCTGCTCTGCTGAGAGAGCCAGCGCTGAGCTTCTTCTTCTTCTCACTCTGAAAGT 212
DB 142 CAGCGCTCTGCTCTGCTGAGAGAGCCAGCGCTGAGCTTCTTCTTCTTCTCACTCTGAAAGT 201
QY 213 GCGAGAGACTACCTGCGCTCTGCGTGAACCAAGCTGCGAGATCCACACTGCTCA 272
DB 202 GCGAGAGACTACCTGCGCTCTGCGTGAACCAAGCTGCGAGATCCACACTGCTCA 261
QY 273 GCTGAGCAATATGAAAAACAAGCTTATGTCGCGATGCTGCTGCTCAACTCTCC 332
DB 262 GCTGAGCAATATGAAAAACAAGCTTATGTCGCGATGCTGCTGCTCAACTCTCC 321
QY 333 TTATGCTCTGCTGCTGCTTCTGCGAGTTCCTCACTCACTCACTGCTCAACTCTCC 392
DB 322 TTATGCTCTGCTGCTGCTTCTGCGAGTTCCTCACTCACTCACTGCTCAACTCTCC 381
QY 393 CTACTATGCGAAGAGAGCTCTGCTGCTTCCAGCGAGCTCTTATCTCACTCACTCT 452
DB 382 CTACTATGCGAAGAGAGCTCTGCTGCTTCCAGCGAGCTCTTATCTCACTCACTCT 441
QY 453 CAAAGAGATGAAGCTTCACTGAGTCTCACTCACTCACTCACTCACTCACTCACT 512
DB 442 CAAAGAGATGAAGCTTCACTGAGTCTCACTCACTCACTCACTCACTCACTCACT 501
QY 513 CCACTTCACTGAG 572
DB 502 CCACTTCACTGAG 561
QY 573 CGTGAAGAGAGCTCTCACTCTCTCTGCTGCTGAGAGAGAGAGAGAGAGAGAG 632
DB 562 CGTGAAGAGAGCTCTCACTCTCTCTGCTGCTGAGAGAGAGAGAGAGAGAGAG 621
QY 633 CAAAG 692
DB 622 CAAAG 681
QY 693 GGGGCAAGAAACAG 752
DB 682 GGGGCAAGAAACAG 741
QY 753 ACAGGGGAGCTAAG 812
DB 742 ACAGGGGAGCTAAG 801
QY 813 GTTTCATCTGAACTCTTATCTTCTCACTCTCTCTCTCTCTCTCTCTCTCTCT 872
DB 802 GTTTCATCTGAACTCTTATCTTCTCACTCTCTCTCTCTCTCTCTCTCTCTCT 861
QY 873 AGAGTCTACTCTATGATATATGAGAAACATCCAGAGCTATTCGATCCAGCCGAG 932
DB 862 AGAGTCTACTCTATGATATATGAGAAACATCCAGAGCTATTCGATCCAGCCGAG 921
QY 933 AGATGAATGAATGAATATATGATGAGAGCTCTCTATGAGAAACCAAAACCTGAG 992
DB 922 AGATGAATGAATGAATATATGATGAGAGCTCTCTATGAGAAACCAAAACCTGAG 981
QY 993 GTTCTGAG 1052
DB 982 CTTCTGAG 1040
QY 1053 TACCTGATCTATTAACCCCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1112
DB 1041 TACCTGATCTATTAACCCCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1100

QY 1113 TTTCCGAGAGCTCGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1172
DB 1101 TTTCCGAGAGCTCGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1160
QY 1173 TGAATTTGCTCTTGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1232
DB 1161 TGAATTTGCTCTTGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1220
QY 1233 ATGGAACCTCCCAAG 1292
DB 1221 ATGGAACCTCCCAAG 1279
QY 1293 CATCGCAACAGAGTGAAGTCCCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1352
DB 1280 CATCGCAACAGAGTGAAGTCCCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1339
QY 1353 TGGGCTTCAATGAG 1412
DB 1340 TGGGCTTCAATGAG 1399
QY 1413 AGTCTGAG 1472
DB 1400 AGTCTGAG 1458
QY 1473 GATTTGAGACAGAGATATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1532
DB 1459 GATTTGAGACAGAGATATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1518
QY 1533 TCTGATGAGAAACCGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1592
DB 1519 TCTGATGAGAAACCGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1578
QY 1593 CAGTGGCTGAG 1652
DB 1579 CAGTGGCTGAG 1638
QY 1653 CACTTGAAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1712
DB 1639 CACTTGAAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1698
QY 1699 ACCTGCGCAAGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1758
DB 1773 CTGTTACTCGGCGCTTCACTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1818
1759 CTGTTACTCGGCGCTTCACTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT

RESULT 8
US-10-653-595-90
Sequence 90, Application US/10653595
Publication No. US2004048304A1
GENERAL INFORMATION:
APPLICANT: Ruben et. al.
TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: P2027P1C1
CURRENT APPLICATION NUMBER: US/10/653,595
PRIOR FILING DATE: 2003-09-03
PRIOR APPLICATION NUMBER: US 09/397945
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: 60/078,566
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR FILING DATE: 1998-03-19

PRIOR APPLICATION NUMBER: 60/080,314
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,312
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-03-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 470
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 90
LENGTH: 1892
TYPE: DNA
ORGANISM: Homo sapiens
US-10-653-595-90

Query Match 67.8%; Score 1284; DB 17; Length 1892;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1794; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

QY 33 CGGATCTTCTCCGCGCATGAGGAGCCAGCCGCTGGCTTCTTCTCCTCACTCTGAAAGT 92
DB 22 CGGATCTTCTCCGCGCATGAGGAGCCAGCCGCTGGCTTCTTCTCCTCACTCTGAAAGT 81
QY 93 GGTGCTCTGCTCTGCGCACTTGCAGCCAGGATTTGCACTCAGGCCCCCACTCAGG 152
DB 82 GGTGCTCTGCTCTGCGCACTTGCAGCCAGGATTTGCACTCAGGCCCCCACTCAGG 141
QY 153 CAGCCCTCTCTCTCTCAACGAAATAGAAAGCTTTTGCACGTGCTCACTCAGG 212
DB 142 CAGCCCTCTCTCTCTCAACGAAATAGAAAGCTTTTGCACGTGCTCACTCAGG 201
QY 213 GCGAGAGCTACCTTCCGCTCTCCGTGCAACCAAGCCGCTGCGGAAATCCCACTGCTCA 272
DB 202 GCGAGAGCTACCTTCCGCTCTCCGTGCAACCAAGCCGCTGCGGAAATCCCACTGCTCA 261
QY 273 GCTGAGCAATATGAAACCAAGCTTATGAGCCCAATGCTGCTCTCAACTCC 332
DB 262 GCTGAGCAATATGAAACCAAGCTTATGAGCCCAATGCTGCTCTCAACTCC 321
QY 333 TTATGCTCTGCTGCTTGAATCTTTTCTGCAATTCATCACTACCTGCTCAACAGT 392
DB 322 TTATGCTCTGCTGCTTGAATCTTTTCTGCAATTCATCACTACCTGCTCAACAGT 381
QY 393 CTATGATGCAAGAGCTCTGTTTCCAGCCAGCTCTATTTCTTCACTCAACTCT 452
DB 382 CTATGATGCAAGAGCTCTGTTTCCAGCCAGCTCTATTTCTTCACTCAACTCT 441
QY 453 CAAGAGATAGAGCTTCAAGCTGTAAGCTCAACCAAGATGCTCTCCCACTCACT 512
DB 442 CAAGAGATAGAGCTTCAAGCTGTAAGCTCAACCAAGATGCTCTCCCACTCACT 501
QY 513 CCACTTCAAGTGAAGAGCCAGACCTTCCAGCCCTGCTGAGAGGCTCAGAACAA 572
DB 502 CCACTTCAAGTGAAGAGCCAGACCTTCCAGCCCTGCTGAGAGGCTCAGAACAA 561
QY 573 CGTGAAGAGCTCTCAATCTCTTCTGCTGCTGAGAGGCTCAGAGCCAGAGAGA 632
DB 562 CGTGAAGAGCTCTCAATCTCTTCTGCTGCTGAGAGGCTCAGAGCCAGAGAGA 621
QY 633 CAAACAGAGAGAGTGAAGCAAGGCAAGAGCCGAGCAAGAAACAAAGCAGAGAGA 692
DB 622 CAAACAGAGAGAGTGAAGCAAGGCAAGAGCCGAGCAAGAAACAAAGCAGAGAGA 681
QY 693 GGGGCAAGAAACAGAGAGAGCAAGAGAGAAAGAGAGAGAGAGAGAGAGAGAG 752
DB 682 GGGGCAAGAAACAGAGAGAGCAAGAGAGAAAGAGAGAGAGAGAGAGAGAGAG 741
QY 753 ACGAGGAGCTAAG 812
DB 742 ACGAGGAGCTAAG 801
QY 813 GTTTCATCTGATCTATCTTCTTCAACCTCTCTCTTCTCCCGGAGTCAAGAGT 872

DB 802 GTTTCATCTGATCTATCTTCTTCAACCTCTCTCTTCTCCCGGAGTCAAGAGT 861
QY 873 AGAGTCTACTCTATAGAAATGAGAAACATCCAGAGCTTATGATGATGAGCCAGAGAA 932
DB 862 AGAGTCTACTCTATAGAAATGAGAAACATCCAGAGCTTATGATGATGAGCCAGAGAA 921
QY 933 AGATGAATGAATGAATATATATGATGAGAACTCTCTGAGAGAAACCAACCTGAGAG 992
DB 922 AGATGAATGAATGAATATATATGATGAGAACTCTCTGAGAGAAACCAACCTGAGAG 981
QY 993 CTCTCTGAGCTGAGCCAGACAGAGCTTCTGCTGCTGCTGCTATGATGATGAGAGAA 1052
DB 982 CTCTCTGAGCTGAGCCAGACAGAG-CCCTTCTGCTGCTGCTGCTATGATGATGAGAGAA 1040
QY 1053 TACTGATCATTAACCCCAAGCCAGAGCTGAGAGTATATGAGAGAGAGAGATCTTGG 1112
DB 1041 TACTGATCATTAACCCCAAGAGCTGAGAGTATATGAGAGAGAGAGATCTTGG 1100
QY 1113 TTTGAGAGAGTGGTCTGAGAGAGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1172
DB 1101 TTTGAGAGAGTGGTCTGAGAGAGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1160
QY 1173 TGAATCTGCTCTTGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1232
DB 1161 TGAATCTGCTCTTGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1220
QY 1233 ATGCGACACTCTCCCAAGAGCTCCCTTGTGAGCCCTTGTGCTGCTCCAGAGCTGTC 1292
DB 1221 ATGCGACACTCTCCCAAGAGCTCCCTTGTGAGCCCTTGTGCTGCTCCAGAGCTGTC 1279
QY 1293 CATGGGCAACAGAGTGGTCCCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1352
DB 1280 CATGGGCAACAGAGTGGTCCCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1339
QY 1353 TGGGCTCACAATGAGCTTGTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1412
DB 1340 TGGGCTCACAATGAGCTTGTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1399
QY 1413 AGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1472
DB 1400 AGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1458
QY 1473 GATTGTGACAGAGCTATATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1532
DB 1459 GATTGTGACAGAGCTATATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1518
QY 1533 TCTGATGAGAAACCGAATCGAGAGAGTCCGCAATGAGATGCTGAGAGAGAGAGAGAG 1592
DB 1519 TCTGATGAGAAACCGAATCGAGAGAGTCCGCAATGAGATGCTGAGAGAGAGAGAGAG 1578
QY 1593 CAGTGGCTGAGCCCTGCAAAAGTGAAGAGTGTGCTTGTGATGAGAGAGAGAGAGAG 1652
DB 1579 CAGTGGCTGAGCCCTGCAAAAGTGAAGAGTGTGCTTGTGATGAGAGAGAGAGAGAG 1638
QY 1653 CACTTGAATCTAGAGAGAGTTCGATGAGAGTGTGATGAGAGAGAGAGAGAGAGAGAG 1712
DB 1639 CACTTGAATCTAGAGAGAGTTCGATGAGAGTGTGATGAGAGAGAGAGAGAGAGAGAG 1698
QY 1713 ACTGAGAGAGTCTATATGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1772
DB 1699 ACTGAGAGAGTCTATATGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1758
QY 1773 CTGTTACTGAG 1832
DB 1759 CTGTTACTGAG 1818

RESULT 9
US-10-296-115-693
Sequence 693, Application US/10296115
Publication No. US20040053248A1
GENERAL INFORMATION:
APPLICANT: Hyseq Inc


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? LENGTH: 964
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 21..527
? FEATURE:
? NAME/KEY: sig_peptide
? LOCATION: 21..95
? OTHER INFORMATION: Von Heijne matrix
? OTHER INFORMATION: score 8.5
? FEATURE:
? NAME/KEY: polyA_signal
? LOCATION: 921..926
? FEATURE:
? NAME/KEY: polyA_site
? LOCATION: 953..963
US-09-978-360A-262

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Query	Match	27.9%	Score 528	DB 11	Length 964
Best Local Similarity	99.3%	Pred. No. 6.4e-268			
Matches 948	Conservative	0	Mismatches 6	Indels 1	Gaps 1
QY	30	GGCGGATCTTCTCCGSCATGAGAGACCGCGCTGCTCTTCCCTCACTCTGAA	89		
DB	2	GGCGGATCTTCTCCGSCATGAGAGACCGCGCTGCTCTTCCCTCACTCTGAA	89		
QY	90	GATGCTGCTCCGCTCTGCGACCTGCGGAGCCGAGATTGACTCAGGCCCCCACTTC	149		
DB	62	GATGCTGCTCCGCTCTGCGACCTGCGGAGCCGAGATTGACTCAGGCCCCCACTTC	149		
QY	150	AGGAGCCCTCTCTCTCTACCGAATACGAGGCTTTTGGACTGTGACTTCAACCTG	121		
DB	122	AGGAGCCCTCTCTCTCTACCGAATACGAGGCTTTTGGACTGTGACTTCAACCTG	209		
QY	210	GAGGAGAGACTACCTCGCGCTCCGTCACCCACGCGTCCGGAAATCCACACTCTG	269		
DB	182	GAGGAGAGACTACCTCGCGCTCCGTCACCCACGCGTCCGGAAATCCACACTCTG	269		
QY	270	CCAGCTGACCAATATGAAAACACAGCGTTAGTACCGAGTGTCTGTCTGCTCAACT	241		
DB	242	CCAGCTGACCAATATGAAAACACAGCGTTAGTACCGAGTGTCTGTCTGCTCAACT	329		
QY	330	CCCTTATGCTCTCTGCTTGTGACTTTTCTGCACTTCACTACGCTGCTCAACCT	301		
DB	302	CCCTTATGCTCTCTGCTTGTGACTTTTCTGCACTTCACTACGCTGCTCAACCT	389		
QY	390	CGTCTACTATCCCAAGAGAGCTCTGTGTTCCAGCCAGTCTTATTTCTCTCAACAC	449		
DB	362	CGTCTACTATCCCAAGAGAGCTCTGTGTTCCAGCCAGTCTTATTTCTCTCAACAC	449		
QY	450	TCTCAAGAGATGAAAGCTTCACTGAACTCACCCACAC-GATGACTTCCCCACTT	508		
DB	422	TCTCAAGAGATGAAAGCTTCACTGAACTCACCCACAC-GATGACTTCCCCACTT	508		
QY	509	CACCCCACTTCAAGTACAGAAACCGCAACCTTCAAGCCTTGAAGAGCTCAGCA	481		
DB	482	CACCCCACTTCAAGTACAGAAACCGCAACCTTCAAGCCTTGAAGAGCTCAGCA	568		
QY	569	ACAACGTGAAAGCTCTTCAATCTCTTCTGCTGAGAGCCGAGGAGCAAGGCCAG	628		
DB	542	ACAACGTGAAAGCTCTTCAATCTCTTCTGCTGAGAGCCGAGGAGCAAGGCCAG	628		
QY	629	AGCAACAACAGAGAGAGAGTGTGAGCAGGCGAGGAGCCGACACAAGAACCAAGCAG	688		
DB	602	AGCAACAACAGAGAGAGAGTGTGAGCAGGCGAGGAGCCGACACAAGAACCAAGCAG	688		
QY	689	AAGAGGGGCGAGAAACAGAGAGAGCAAGAGAGAAACAGAGAGGAGGAAAGCAGAG	748		
DB	662	AAGAGGGGCGAGAAACAGAGAGAGCAAGAGAGAAACAGAGAGGAGGAAAGCAGAG	748		
QY	749	AAGAGAGGCGAGCTAAGAGAGGAGCGGAGGCTGTCTCACTGAGACAGACTCAAGC	808		

Db 722 AAGCAGCGGAGCTAAGAGGAGGAGGCTGTGTCTACCTCAGACAGACTCAGAC 78
Qy 809 CCAAGTTTCACTCTGAATCTCTATCTTCTTAACCCCTCTCTTTTGTCTCCCCGGTAGAG 86
Db 782 CCAAGTTTCACTCTGAATCTCTATCTTCTTAACCCCTCTCTTTTGTCTCCCCGGTAGAG 84
Qy 869 AAGTAGAGTCTACTCTCTATATATATAGAGACATCCAGAGCTCATTCGATCAGCCAG 92
Db 842 AAGTAGAGTCTACTCTATATATATAGAGACATCCAGAGCTCATTCGATCAGCCAG 90
Qy 929 AATATGATGAATGAAATATATATAGTAGGAATCTCTTCTAGAGAAACCAAA 98
Db 902 AATATGATGAATGAAATGAAATATATATAGTAGGAATCTCTTCTAGAGAAACCAAA 95

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RESULTS
US-10-719-993-6794
; Sequence 6794, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICATION:

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1  INVENTOR: CARGILL, Michele et al.
2  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
3  TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
4  FILE REFERENCE: CL001496
5  CURRENT APPLICATION NUMBER: US/10/719,993
6  CURRENT FILING DATE: 2003-11-24
7  NUMBER OF SEQ ID NOS: 55342
8  SOFTWARE: FastSeq for Windows Version 4.0
9  SEQ ID NO 6794
10 LENGTH: 21347
11 TYPE: DNA
12 ORGANISM: Homo sapiens
13 us-10-719-993-6794

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Query Match	24.9%	Score 471;	DB 18;	Length 21347;
Best Local Similarity	100.0%;	Pred. No.	7.1e-238;	
Matches 471; Conservation				

	Qy	Indels	Gaps
322	AATGACAGAACGCCAGACTTTCACAGCCCTTGGCTTGAGAGCTTCAGACCAACAGCTGGAGA	0	0
Db	8812	AATGACAGAACGCCAGACTTTCAGAGCCCTTGGCTTGAGAGCTTCAGACCAACAGCTGGAGA	581
Qy	582	GCTCCTCAATACCTCCCTTGTCTTGGAGGCTCCAGAGCAGAGCCGACAGACCAAGCAGCA	88712
Db	8872	GCTCCTCAATACCTCCCTTGTCTTGGAGGCTCCAGAGCAGAGCCGACAGACCAAGCAGCA	88712
Qy	642	GCAAGAGTGTGAGCAACAGCAGAGACCCGACACAAAGACCAAGCAGAGAGAGGGGACGAA	89311
Db	8932	GCAAGAGTGTGAGCAACAGCAGAGACCCGACACAAAGACCAAGCAGAGAGAGGGGACGAA	701
Qy	702	ACAGGAAGACGAAGAGAGAGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	8991
Db	8992	ACAGGAAGACGAAGAGAGAGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	761
Qy	762	TAAAGAGGACCGGAGGCTGTGTCTCAAGCTGACAGACAGACTTCAGAGCCCAAGTTTCAC	9051
Db	9052	TAAAGAGGACCGGAGGCTGTGTCTCAAGCTGACAGACAGACTTCAGAGCCCAAGTTTCAC	821
Qy	822	TGAATCTCTATCTTCTTAAACCTTCCCTCTTTTGGTCCCGGAGTACAGAGAGTGAAGTCTAC	9111
Db	9112	TGAATCTCTATCTTCTTAAACCTTCCCTCTTTTGGTCCCGGAGTACAGAGAGTGAAGTCTAC	881
Qy	882	TCCTATGATATGAGAGAACATCCAGAGCTCACTTGATCAGCCACGAGAAATAGATGAAAT	9171
Db	9172	TCCTATGATATGAGAGAACATCCAGAGCTCACTTGATCAGCCACGAGAAATAGATGAAAT	941
Qy	942	GAATGAAATATATGAGAGAACTCTTACTGTGAGAAACCAAAACCTGTGGCAG	9231
Db	9232	GAATGAAATATATGAGAGAACTCTTACTGTGAGAAACCAAAACCTGTGGCAG	9282

US-10-085-117-52
; Sequence 52, Application US/10085117
; Publication No. US2003023234A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David M.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 29346
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)...(29346)
; OTHER INFORMATION: n = any nucleotide
US-10-085-117-52

Query Match 24.9%; Score 471; DB 17; Length 29346;
Best Local Similarity 100.0%; Pred. No. 7e-238;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 AGTGAAGAAAGCGCAAGCTTCCAGCCCTGAGAGGCTCAGCAACAGCTGGAAGA 581
DB 12812 AGTGAAGAAAGCGCAAGCTTCCAGCCCTGAGAGGCTCAGCAACAGCTGGAAGA 12871
QY 582 GCTCCCAACATCCTCTGTGCTGAGAGGCGCAAGAGCGCCAGAGCAAGCAAGCA 641
DB 12872 GCTCCCAACATCCTCTGTGCTGAGAGGCGCAAGAGCGCCAGAGCAAGCAAGCA 12931
QY 642 GCAGAGAGTGAAGCAAGGAGGAGCGCAAGCAAGCAAGCAAGCAAGGAGGAGCA 701
DB 12932 GCAGAGAGTGAAGCAAGGAGGAGCGCAAGCAAGCAAGCAAGCAAGGAGGAGCA 12991
QY 702 ACAGAGAGCAAGAGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 761
DB 12992 ACAGAGAGCAAGAGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 13051
QY 762 TAAG 821
DB 13052 TAAG 13111
QY 822 TGAATCTCTATCTTCTAACCCTCTCTTTTGTCTCCCGGGTACAGAGAGTAC 881
DB 13112 TGAATCTCTATCTTCTAACCCTCTCTTTTGTCTCCCGGGTACAGAGAGTAC 13171
QY 882 TCCTATGATATGAG 941
DB 13172 TCCTATGATATGAG 13231
QY 942 GATGAG 992
DB 13232 GATGAG 13282

RESULT 13
US-09-918-995-14842
; Sequence 14842, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076

; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14842
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(469)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-14842

Query Match 20.0%; Score 379; DB 10; Length 469;
Best Local Similarity 99.8%; Pred. No. 3.6e-189;
Matches 429; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 936 TGAATGAATGAAT 995
DB 40 TGAATGAATGAAT 99
QY 996 CTTGAG 1055
DB 100 CTTGAG 159
QY 1056 CTGATCATATACCCCAAG 1115
DB 160 CTGATCATATACCCCAAG 219
QY 1116 CGGAG 1175
DB 220 CGGAG 279
QY 1176 CTTCCTCTCTTGAAG 1235
DB 280 CTTCCTCTCTTGAAG 339
QY 1236 CGAG 1295
DB 340 CGAG 399
QY 1296 CGGAG 1355
DB 400 CGGAG 459
QY 1356 GCTCCACATG 1365
DB 460 GCTCCACATG 469

RESULT 14
US-10-719-993-7043
; Sequence 7043, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7043
; LENGTH: 24923
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(24923)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-;
US-10-719-993-7043

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2005, 08:49:26 ; Search time 338 Seconds
(without alignments)
9173.800 Million cell updates/sec

Title: US-09-559-013E-23

Perfect score: 1895
Sequence: 1 gttagagcggtctgtctcc.....tgtgattctcaaaaaaa 1895

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapept 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents NA:*

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2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
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5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	258.8	13.7	316	4 US-09-621-976-3396	Sequence 3396, App1
2	75.2	4.0	7218	1 US-08-232-463-14	Sequence 14, App1
3	73.4	3.9	51259	3 US-08-781-891-209	Sequence 209, App1
4	73.4	3.9	51259	4 US-09-618-166-209	Sequence 209, App1
5	72.6	3.8	16442	3 US-08-781-891-208	Sequence 208, App1
6	72.6	3.8	16442	4 US-09-618-166-208	Sequence 208, App1
7	72.2	3.8	12635	4 US-09-949-016-16775	Sequence 16775, A
8	71.2	3.8	1926	3 US-09-249-585A-2	Sequence 2, App1
9	71.2	3.8	1926	4 US-09-410-399-3	Sequence 3, App1
10	71.2	3.8	2580	3 US-09-050-863-2	Sequence 2, App1
11	71.2	3.8	2580	4 US-09-359-081-2	Sequence 2, App1
12	71.2	3.8	5452	2 US-09-130-114-1	Sequence 1, App1
13	71.2	3.8	8705	4 US-09-647-344A-14	Sequence 14, App1
14	71.2	3.8	9600	3 US-08-910-647-1	Sequence 1, App1
15	71.2	3.8	9600	3 US-09-620-925-1	Sequence 1, App1
16	71.2	3.8	10596	1 US-07-884-811-15	Sequence 15, App1
17	71.2	3.8	10596	1 US-07-885-971-15	Sequence 15, App1
18	71.2	3.8	10596	1 US-08-087-783A-15	Sequence 15, App1
19	71.2	3.8	10596	1 US-08-194-088B-15	Sequence 15, App1
20	71.2	3.8	10596	2 US-08-194-088B-15	Sequence 15, App1
21	71.2	3.8	10596	5 PCT-US93-04648-15	Sequence 15, App1
22	71.2	3.8	16080	4 US-09-724-566A-48	Sequence 48, App1
23	71.2	3.8	16080	4 US-09-471-669A-48	Sequence 48, App1
24	68.6	3.6	3489	3 US-08-728-123A-1	Sequence 1, App1
25	68.6	3.6	3489	3 US-09-298-568-1	Sequence 1, App1
26	68.6	3.6	3489	3 US-09-410-599-1	Sequence 1, App1
27	68.6	3.6	3489	4 US-09-894-273-1	Sequence 1, App1

C 28	68.6	3.6	32207	2 US-08-770-379-20	Sequence 20, App1
C 29	68.6	3.6	32207	3 US-08-757-669A-20	Sequence 20, App1
C 30	68.6	3.6	32207	3 US-09-230-371A-20	Sequence 20, App1
C 31	67.8	3.6	816	4 US-09-248-796A-6947	Sequence 6947, App1
C 32	66.8	3.5	2301	1 US-08-306-691B-23	Sequence 23, App1
C 33	66.8	3.5	2301	4 US-09-167-206-3	Sequence 3, App1
C 34	66.8	3.5	2301	5 PCT-US93-06251-78	Sequence 78, App1
C 35	66	3.5	194937	4 US-09-949-016-17032	Sequence 17032, A
C 36	66	3.5	194937	4 US-09-949-016-17033	Sequence 17033, A
C 37	64.4	3.4	72549	4 US-09-949-016-16477	Sequence 16477, A
C 38	63.8	3.4	85850	4 US-09-949-016-13424	Sequence 13424, A
C 39	61.8	3.3	289	3 US-09-007-005-17	Sequence 17, App1
C 40	61.8	3.3	289	3 US-09-244-796-17	Sequence 17, App1
C 41	61.2	3.2	601	4 US-09-949-016-90371	Sequence 90371, A
C 42	60.4	3.2	247781	4 US-09-949-016-14193	Sequence 14193, A
C 43	60	3.2	18798	4 US-09-949-016-14339	Sequence 14339, A
C 44	59.6	3.1	601	4 US-09-949-016-90372	Sequence 90372, A
C 45	59.6	3.1	96340	4 US-09-949-016-15863	Sequence 15863, A

ALIGNMENTS

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RESULT 1
US-09-621-976-3396
; Sequence 3396, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3396
; LENGTH: 316
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 66..311
; NAME/KEY: misc_feature
; LOCATION: 301
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-3396

```

Query Match 13.7%; Score 258.8; DB 4; Length 316;
Best Local Similarity 96.0%; Pred. No. 2.8e-64;
Matches 291; Conservative 5; Mismatches 3; Indels 4; Gaps 3;

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QY 1 GTTAGAGGCGGCTGTGTCTCAGCGGAGCGGGCGATCTTTCGGCCATGAGAAACCA 60
DB GTTAGAGGCGGCTGTGTCTCAGCGGAGCGGGCGATCTTTCGGCCATGAGAAACCA 77
QY 61 GCGGCTGGCTCTCTTCTCTCAGCGGAGCGGGCGATCTTTCGGCCATGAGAAACCA 120
DB GCGGCTGGCTCTCTTCTCTCAGCGGAGCGGGCGATCTTTCGGCCATGAGAAACCA 134
QY 121 GCCCAGATTCGACTGAGGCGCCCACTCCAGGAGCGGCTCTCTCTGACCAATACGAA 180
DB GCCCAGATTCGACTGAGGCGCCCACTCCAGGAGCGGCTCTCTCTGACCAATACGAA 194
QY 181 CGCTTTCGCACTGCTGACTCCAACTGAGAGAGAGACTACCTGCTCCGTCGCA 240
DB CGCTTTCGCACTGCTGACTCCAACTGAGAGAGAGACTACCTGCTCCGTCGCA 253
QY 241 ACCCAGGCGTCCGAGATCCCACTGCTGAGCTGAGCAATATGAAAAACGAGCTTA 300
DB ACCCAGGCGTCCGAGATCCCACTGCTGAGCTGAGCAATATGAAAAACGAGCTTA 313

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4
C
A

147 AGGAG

[illegible]

us-09-559-013e-23.rtf

TITLE OF INVENTION: Schellenberg, Gerald D.
 NUMBER OF SEQUENCES: GENE AND GENE PRODUCTS RELATED TO
 WERNER'S SYNDROME
 CORRESPONDENCE ADDRESS: 209
 ADDRESS: Seed Intellectual Property Law Group
 STREET: 701 Fifth Avenue, Suite 6300
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/618,166
 FILING DATE: 17-Jul-2000
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: McMasters, David D.
 REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 240052.419C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 208:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16442 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 208:

[illegible]

RESULT 7
 US-09-949-016-16775/c
 Sequence 16775, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 CURRENT APPLICATION NUMBER: CL001307
 CURRENT FILING DATE: US/09/949,016
 PRIOR APPLICATION NUMBER: 2000-04-14
 PRIOR FILING DATE: 2000-04-14, 755
 PRIOR APPLICATION NUMBER: 2000-10-20
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498

	Query Match	3.8%	Score 72.2	DB 4	Length 12695
	Best Local Similarity	55.9%	Prid. No. 1.4e-09		
	Matches 137	Conservative 0	Mismatches 108	Indels 0	Gaps 0
Qy	563	TCAGCAACACGTGGAGAGCTCTCAATCTCTTGTCTCTTGGAGGCGCAGAGCAAG	622		
Db	9739	TCAGTGAAGCCAGGACCAAGACATCTCACTTAGGCTGAGAGAGAGAAAGAGAGAGAG	9681		
Qy	623	CGCCAGAGCACAAGCAGAGGCACAAAGATGTGAGCA	CAGGCGAGAGCCGACACAAGAACACA	682	
Db	9679	AGAGAGAGGAAAGAGAGAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	9679		
Qy	683	AGCAGGAAGAGGCGCAGAAACAGAAAGCACAAGAAAGGAAACAGAAAGAGAGGAGAAAGC	742		
Db	9619	AGGAAAG	9560		
Qy	743	AGGAAAG	9560		
Db	9559	AGGAAAG	9559		
Qy	803	CAGAG 807			
Db	9499	AGGAG 9495			

```

RESULT 8
US-09-249-585A-2
/ Sequence 2, Application US/09249585A
/ Patent No. 6417002
/ GENERAL INFORMATION:
/ APPLICANT: HOLLICK, Robert
/ TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
/ FILE REFERENCE: 0867/0D905
/ CURRENT APPLICATION NUMBER: US/09/249,585A
/ NUMBER FILING DATE: 1999-02-11
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 2
/ LENGTH: 1926
/ TYPE: DNA
/ ORGANISM: Epstein Barr Virus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(1926)
/ OTHER INFORMATION: coding strand of EBNA-1 DNA
US-09-249-585A-2

```

[illegible]

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-359-081-2

Query Match
Best Local Similarity 61.2%; Score 71.2; DB 3; Length 2580;
Matches 115; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

613 CAGGAGCAAGCCGACGACCAAGCAGAGCAGAGCAAGAGTGAAGCAAGGCGAGGAGCCGACA 672
DB CAGGAGGAGGGGCGAGAGCAGAGGAGGAGGCGAGAGCGAGGCGAGGAGGCGAGGAGG 819
QY 673 CAGGAGCAAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 819
DB 820 GAGGGGCGAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 879
QY 733 GAGGAGAAAGCAGAGAGAGAGCAGAGGAGCTTAAGAGAGGAGCGGAGGCTGTCTCACTG 792
DB 880 CAGGAGGGGCGAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 939
QY 793 CAGAGAGA 800
DB 940 CAGAGAGA 947

RESULT 12

US-09-130-114-1/C
Sequence 1, Application US/09130114
Patent No. 5976807
GENERAL INFORMATION:
APPLICANT: Horlick, Robert A.
APPLICANT: Dama, Basam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
FILE REFERENCE: 0867/ID903US1
CURRENT APPLICATION NUMBER: US/09/130.114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 5452
TYPE: DNA
ORGANISM: VEBNA
US-09-130-114-1

Query Match
Best Local Similarity 61.2%; Score 71.2; DB 2; Length 5452;
Matches 115; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

613 CAGGAGCAAGCCGACGACCAAGCAGAGCAGAGTGAAGCAAGGCGAGGAGCCGACA 672
DB 2045 CAGGAGGAGGGGCGAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1986
QY 673 CAGGAGCAAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 732
DB 1985 GAGGGGCGAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1926
QY 733 GAGGAGAAAGCAGAGAGAGAGCAGAGGAGCTTAAGAGAGGAGCGGAGGCTGTCTCACTG 792
DB 1925 CAGGAGGGGCGAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1866
QY 793 CAGAGAGA 800
DB 1865 CAGAGAGA 1858

RESULT 13

US-09-647-344A-14/C
Sequence 14, Application US/09647344A
Patent No. 6586180
GENERAL INFORMATION:
APPLICANT: Ruffner, Duane E.
APPLICANT: Pierce, Michael L.
APPLICANT: Chen, Zhidong
TITLE OF INVENTION: Directed Antisense Libraries
FILE REFERENCE: 16678.PCT.US
CURRENT APPLICATION NUMBER: US/09/647.344A
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: PCT/US99/06742
PRIOR FILING DATE: 1999-03-28
NUMBER OF SEQ ID NOS: 50
SEQ ID NO 14
LENGTH: 8705
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pshuttle
US-09-647-344A-14

Query Match
Best Local Similarity 61.2%; Score 71.2; DB 4; Length 8705;
Matches 115; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

613 CAGGAGCAAGCCGACGACCAAGCAGAGCAGAGTGAAGCAAGGCGAGGAGCCGACA 672
DB 7910 CAGGAGGAGGGGCGAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7851
QY 673 CAGGAGCAAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 732
DB 7850 GAGGGGCGAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7791
QY 733 GAGGAGAAAGCAGAGAGAGAGCAGAGGAGCTTAAGAGAGGAGCGGAGGCTGTCTCACTG 792
DB 7790 CAGGAGGGGCGAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7731
QY 793 CAGAGAGA 800
DB 7730 CAGAGAGA 7723

RESULT 14

US-08-910-647-1
Sequence 1, Application US/08910647
Patent No. 6251433
GENERAL INFORMATION:
APPLICANT: Zuckermann et al.
TITLE OF INVENTION: Compositions and Methods for
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910.647
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1218.002

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XX 01-DEC-2000; 2000WO-US032750.
 PF 01-DEC-1999; 99US-016833P.
 PR 26-APR-2000; 2000US-00559013.
 XX (LUDWIG INST CANCER RES.
 PA Ono T, Nakayama E;
 PI WPI, 2001-397941/42.
 DR P-PSDB; AAE04382.
 XX
 PT Isolated polypeptide, useful in treating disorders such as cancer, is
 PT encoded by a nucleic acid (NA) Group 3 or 4 molecule.
 PS Claim 56; Fig 2; 127pp; English.
 CC The invention relates to cancer associated antigens and their nucleic
 CC acids which are expressed in methylcholanthrene-induced fibrosarcoma
 CC cancer cells from mice. Cancer associated antigens and a pharmacoma
 CC composition containing nucleic acid molecules encoding cancer associated
 CC antigens are used to treat a condition e.g. cancer. Cancer associated
 CC antigens, the nucleotides encoding them, antibodies against them and the
 CC monitoring and treating the diseases characterised by the expression of
 CC one or more cancer associated antigens, e.g. fibrosarcoma cancer, and for
 CC research purposes. Cancer associated antigens DNA is also useful in gene
 CC therapy. The present sequence is a cDNA encoding human cancer associated
 CC antigen OY-TES-1
 XX

Sequence 1895 BP; 449 A; 565 C; 481 G; 400 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1895; DB 5; Length 1895;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1895; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTAGAGGCGGCTTGTGTCCAGGAGCGGCGGATCTTCCGGCCATAGGAAGCA 60
 DB 1 GTTAGAGGCGGCTTGTGTCCAGGAGCGGCGGATCTTCCGGCCATAGGAAGCA 60
 OY 61 GCGGCTGCTTCTTCTCTCACTCTGTAAGGTCGTCTGCTTCTTCCGATAGGAAGCA 60
 DB 61 GCGGCTGCTTCTTCTCTCACTCTGTAAGGTCGTCTGCTTCTTCCGATAGGAAGCA 60
 OY 121 GCCCAGATTGCACTCAGGCCCCCACTCAGGAGCCCTCTCTCTCAAGAAACGAA 180
 DB 121 GCCCAGATTGCACTCAGGCCCCCACTCAGGAGCCCTCTCTCTCAAGAAACGAA 180
 OY 181 GCGTCTTGTGACCTGCTGACCTCAACCTGGAAGGAGAGACTACGCGCTCCGTCGA 240
 DB 181 GCGTCTTGTGACCTGCTGACCTCAACCTGGAAGGAGAGACTACGCGCTCCGTCGA 240
 OY 241 ACCCAGGCTGCGGAATCCCACTGTCACAGTGAACCAATATGAAACACAGGCTTA 300
 DB 241 ACCCAGGCTGCGGAATCCCACTGTCACAGTGAACCAATATGAAACACAGGCTTA 300
 OY 301 GTGCCAGATGCTGTCTGCTCAACCTCTTATGCTCCCGGTTGAAGCTTTCTGCG 360
 DB 301 GTGCCAGATGCTGTCTGCTCAACCTCTTATGCTCCCGGTTGAAGCTTTCTGCG 360
 OY 361 CAGTTCACCTACCTGCTGCTCAACAGCTCTACTATGCAAGAGAGTCTGTGTTCC 420
 DB 361 CAGTTCACCTACCTGCTGCTCAACAGCTCTACTATGCAAGAGAGTCTGTGTTCC 420
 OY 421 CAGCAGCTCTTATTTCTGACCTTAACCTCTCAAGAGATGAAAGCTTCAAGTTC 480
 DB 421 CAGCAGCTCTTATTTCTGACCTTAACCTCTCAAGAGATGAAAGCTTCAAGTTC 480
 OY 481 TCACCCACCAAGATGCTGCTCCCACTCAACCCACTTCAAGTGAAGAGAGCCAGACC 540
 DB 481 TCACCCACCAAGATGCTGCTCCCACTCAACCCACTTCAAGTGAAGAGAGCCAGACC 540

OY 541 TTCAGCCCTGCGCTGAGAGGCTCAGCAACACTGTAAGAGCTCTTACATCTCTTGG 600
 DB 541 TTCAGCCCTGCGCTGAGAGGCTCAGCAACACTGTAAGAGCTCTTACATCTCTTGG 600
 OY 601 TCCCTGGAGGCTCAGAGCAAGCCAGAGCAACAGAGAGAGAGAGAGAGAGAGAG 660
 DB 601 TCCCTGGAGGCTCAGAGCAAGCCAGAGCAACAGAGAGAGAGAGAGAGAGAGAG 660
 OY 661 CAGAGCCGACACAAAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 DB 661 CAGAGCCGACACAAAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 OY 721 GAACAGGAAG 780
 DB 721 GAACAGGAAG 780
 OY 781 GTGTCTAGCTGACAGACAGCTCAGAGCCCAAGTTTCACTGATCTCTTCTTAC 840
 DB 781 GTGTCTAGCTGACAGACAGCTCAGAGCCCAAGTTTCACTGATCTCTTCTTAC 840
 OY 841 CTTTCTCTTTTCT 900
 DB 841 CTTTCTCTTTTCT 900
 OY 901 ATCCAGAGCTTATTCATCAGTCCAGAGAAATGATGAATGAATGAATGAATGA 960
 DB 901 ATCCAGAGCTTATTCATCAGTCCAGAGAAATGATGAATGAATGAATGAATGA 960
 OY 961 AACTCTACTGGAAGAAACAAACCTCGAGCTTCTCGAGCTGCCCCACAGAGGCG 1020
 DB 961 AACTCTACTGGAAGAAACAAACCTCGAGCTTCTCGAGCTGCCCCACAGAGGCG 1020
 OY 1021 TTGCTGTGCTGTGCTATTCATGATGAGAGATTCCTGATTAACCCCAAGCAAG 1080
 DB 1021 TTGCTGTGCTGTGCTATTCATGATGAGAGATTCCTGATTAACCCCAAGCAAG 1080
 OY 1081 GCTTGAAGATGATGAGAGAGAGAGATTCCTGATTAACCCCAAGCAAGCAAG 1140
 DB 1081 GCTTGAAGATGATGAGAGAGAGAGATTCCTGATTAACCCCAAGCAAGCAAG 1140
 OY 1141 GGGGCGGACATATGCTTACTGTGCTCTGTGATCTTGTGATGAGAGAGAG 1200
 DB 1141 GGGGCGGACATATGCTTACTGTGCTCTGTGATCTTGTGATGAGAGAGAG 1200
 OY 1201 TGCCACTCAGAGGCGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
 DB 1201 TGCCACTCAGAGGCGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
 OY 1261 GTGAGCCCTTGTGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
 DB 1261 GTGAGCCCTTGTGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
 OY 1321 TCAGGCGGCTTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
 DB 1321 TCAGGCGGCTTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
 OY 1381 CCGCTTGGCAAGAAAGGCTGGAAGATGTCAGAGCTCTGAGAGAGAGAGAGAG 1440
 DB 1381 CCGCTTGGCAAGAAAGGCTGGAAGATGTCAGAGCTCTGAGAGAGAGAGAGAG 1440
 OY 1441 CTTAGCTTCAAG 1500
 DB 1441 CTTAGCTTCAAG 1500
 OY 1501 CCAAACTACTGTTCTTCAAAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
 DB 1501 CCAAACTACTGTTCTTCAAAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
 OY 1561 TCCCGATGAGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
 DB 1561 TCCCGATGAGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
 OY 1621 GAGGTGTGCTTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680

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Db      1621 GAGGTGTGCTTGATGAGACCGAGAGTTCAGACCTTGACTGAGCCAGTTGAGATGA 1680
Qy      1681 GCTGGAGCTATCTGCGCACACCCGAGCCCACTGCGCCAGCTTCTATTGTTTGG 1740
Db      1681 GCTGGAGCTATCTGCGCACACCCGAGCCCACTGCGCCAGCTTCTATTGTTTGG 1740
Qy      1741 ACCCATTTGCTTTCAGGCTGCGCTTCTGAGTCTGTTACTGCGCCCTACTACATTTC 1800
Db      1741 ACCCATTTGCTTTCAGGCTGCGCTTCTGAGTCTGTTACTGCGCCCTACTACATTTC 1800
Qy      1801 TTGGGTTGAGCAACAGTCCCAAGAGAGGCGCAGGTGGAGCTGCGCCCTCTTAAAGA 1860
Db      1801 TTGGGTTGAGCAACAGTCCCAAGAGAGGCGCAGGTGGAGCTGCGCCCTCTTAAAGA 1860
Qy      1861 TGACTTACATAAATGTGTGATCTTCAAAAAA 1895
Db      1861 TGACTTACATAAATGTGTGATCTTCAAAAAA 1895

```

RESULT 2

AAZ50927 standard; cDNA; 1912 BP.

AAZ50927; 05-JUN-2000 (first entry)

Human Protease and associated protein-10 (PPRG-10) encoding cDNA.

Protease and associated protein-10; PPRG-10; anti-PPRG antibody;
 diagnosis; treatment; cell proliferative disorder; cancer; cirrhosis;
 arteriosclerosis; atherosclerosis; bursitis; hepatitis; immune disorder;
 AIDS; Addison's disease; adult respiratory distress syndrome; allergy;
 ankylosing spondylitis; amyloidosis; cytostatic; antiarteriosclerotic;
 hepatocellular; antiinflammatory; virucide; antiposrotic; anti-HIV;
 antiallergic; immunosuppressive; antidiabetic; antianaemic;
 neuroprotective; human; ss.

Homo sapiens.

Location/Qualifiers

Key CDS

/tag= a

/product= "Human PPRG-10"

/tag= b

/tag= c

/product= "Mature PPRG-10"

/tag= d

/bound_moiety= "Probe or Primer"

WO200009709-A2.

24-FEB-2000.

06-AUG-1999; 99WO-US017818.

10-AUG-1998; 98US-0096114P.

11-FEB-1999; 99US-0119768P.

(INCY-) INCYTE PHARM INC.

Bandman O, Hillman JL, Baughn MR, Aizmai Y, Guejler KJ;

Corley NC, Yue H, Tang YT, Reddy R, Patterson C, Au-Young J;

Shih LL, Lu DM;

WPI; 2000-224346/19.

P-PDB; AAY70016.

New human proteases, useful for diagnosis, treatment and prevention of

PT cell proliferative disorders such as atherosclerosis.
 XX Claim 9; Page 106; 114pp; English.

CC The present sequence is a cDNA identified in Incyte clone 1393301 derived
 CC from THYNOT03 cDNA library. It encodes human protease and associated
 CC protein-10 (PPRG-10), which is expressed in reproductive, endocrine,
 CC hematopoietic and immune tissues. Anti-PPRG antibodies can be used as
 CC therapeutic antagonists, reagents for diagnosis and monitoring diseases
 CC and for isolating PPRG. PPRG nucleotide sequence can be used as probe or
 CC primer for diagnosis and monitoring of PPRG-related diseases and gene
 CC mapping. PPRG can be used in the treatment of cell proliferative
 CC disorders like cancer, arteriosclerosis, atherosclerosis, bursitis,
 CC cirrhosis and hepatitis, and immune disorders like AIDS, Addison's
 CC disease, adult respiratory distress syndrome, allergies, ankylosing
 CC spondylitis and amyloidosis

Sequence 1912 BP; 455 A; 567 C; 487 G; 403 T; 0 U; 0 Other;

Query Match 99.7%; Score 1890.2; DB 3; Length 1912;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1892; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 GTTAGAGCGCGCTTGTGTCCAGCGAGCGCGGATCTTCTCCGCGCATGAGGAGCCA 60
Db      17 GTTAGAGCGCGCTTGTGTCCAGCGAGCGCGGATCTTCTCCGCGCATGAGGAGCCA 76
Qy      61 GCGCGTGGCTTCTCCCTCCCTCAGTCCAGAGTGTCTGCTGCTGCGACCTGCGCA 120
Db      77 GCGCGTGGCTTCTCCCTCCCTCAGTCCAGAGTGTCTGCTGCTGCGACCTGCGCA 136
Qy      121 GCCCAGAGTTCAGTCAAGCGCCCACTCCAGAGCGCTCTCTCTCAAGATAGAA 180
Db      137 GCCCAGAGTTCAGTCAAGCGCTCCATCCAGAGCGCTCTCTCTCAAGATAGAA 196
Qy      181 CGCTTCTGCGACTGCTGACTCCAACTGAGAGGCAAGACTACCTGCTTCCGTGCA 240
Db      197 CGCTTCTGCGACTGCTGACTCCAACTGAGAGGCAAGACTACCTGCTTCCGTGCA 256
Qy      241 ACCCAGCGCTGCGGAGTCCCACTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCC 300
Db      257 ACCCAGCGCTGCGGAGTCCCACTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCC 316
Qy      301 GTGCGGATGTGTGTCTGCTCTCAACTCACTCTCAAGAGATAGAGTTCAGTGAAGTC 360
Db      317 GTGCGGATGTGTGTCTGCTCTCAACTCACTCTCAAGAGATAGAGTTCAGTGAAGTC 376
Qy      361 CAGTTCACTCACTACCGTTGCTCCAAACAGCTCTATGCAAGAGAGTCTGTGTTCC 420
Db      377 CAGTTCACTCACTACCGTTGCTCCAAACAGCTCTATGCAAGAGAGTCTGTGTTCC 436
Qy      421 CAGCAGTCTCTATTCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 480
Db      437 CAGCAGTCTCTATTCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 496
Qy      481 TCACCCACAGAGTACCTCCCATCTCACTCACTCACTCACTCACTCACTCACTCACTCA 540
Db      497 TCACCCACAGAGTACCTCCCATCTCACTCACTCACTCACTCACTCACTCACTCACTCA 556
Qy      541 TTCACGCTTGGCTGAGAGGCTCAGCAACAGTGGAGAGTCTTCAATCTCTCTTG 600
Db      557 TTCACGCTTGGCTGAGAGGCTCAGCAACAGTGGAGAGTCTTCAATCTCTCTTG 616
Qy      601 TCCCTGGAGGCGAGAGGAGGCGCAGAGCAACAGAGAGAGAGAGAGAGAGAGAG 660
Db      617 TCCCTGGAGGCGAGAGGAGGCGCAGAGCAACAGAGAGAGAGAGAGAGAGAGAG 676
Qy      661 CAGAGCCGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db      677 CAGAGCCGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 736
Qy      721 GAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780

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PD 23-DEC-1998.

XX 18-JUN-1998; 98WC-US012516.

PR 19-JUN-1997; 97US-00878715.

PR 17-JUN-1998; 98US-00098588.

PA (GENE) GENETICS INST INC.

PI Jacobs K, McCoy JM, Lavallie ER, Racine LA, Treacy M, Spaulding V, Agostino MJ, Howes SH, Fechtel K;

DR MPI; 1999-095321/08.

XX P-PSDB; AAM88403.

PS Claim 24(a); Page 84-85; 122pp; English.

This cDNA clone, termed 9a63.6, codes for a novel human secreted protein (see AAM88403). The full-length clone was isolated from a human adult testis cDNA library using methods which are selective for cDNAs encoding secreted proteins, or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. Its sequence shows at least some similarity to some known database sequences. The invention provides cDNA clones (see AAX06780-89) from human adult testis, foetal brain, adult uterus, adult trachea and adult neural tissue that encode novel secreted proteins (see AAM88398-407). The clones are deposited as ATCC 96468, from which each can be isolated using specified probes (see AAX06790-99). The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional, cytokine, cell proliferation/differentiation, immune stimulating (e.g. as vaccines) or inhibiting, haematopoiesis regulation, tissue growth, activation or inhibition, chemotactic or chemokinetic, haemostatic, thrombolytic activity, and tumour inhibition activities. The polynucleotides are also stated to be useful for gene therapy, and for recombinant production of the claimed proteins.

Sequence 1899 BP; 457 A; 560 C; 477 G; 401 T; 0 U; 4 Other;

Query Match 98.0%; Score 1856.4; DB 2; Length 1899; Best Local Similarity 99.4%; Pred. No. 0; Matches 1879; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

QY 7 GCGCGCTGTGTCACCGGAGCGCGGATCTTCTCCGCGCATGAGAGCCAGCCGCT 66
DB 1 GCGCGCTGTGTCACCGGAGCGCGGATCTTCTCCGCGCATGAGAGCCAGCCGCT 66
QY 67 GCGCTTCTTCTCTGATGAGTCTCTGCTGTCGACCTGCGGACCGGACCGGAC 126
DB 61 GCGCTTCTTCTCTGATGAGTCTCTGCTGTCGACCTGCGGACCGGACCGGAC 126
QY 127 GATTGCACTAGGCGCCCACTCCAGGAGCGCTCTCTCTCTTACCGAATACGAGCTTC 186
DB 121 GATTGCACTAGGCGCT 180
QY 187 TTGCGACTGCTGACTCCAACTGGAAGGAGAGACTACTGCGGCTCCGCTCCGCAACCCAC 246
DB 181 TTGCGACTGCTGACTCCAACTGGAAGGAGAGACTACTGCGGCTCCGCTCCGCAACCCAC 246
QY 247 GCGTGCAGGAATCCGACACTCGTCCGCTGAGCAATATGAAACAGCGCTTAGTGC 306
DB 241 GCGTGCAGGAATCCGACACTCGTCCGCTGAGCAATATGAAACAGCGCTTAGTGC 306
QY 307 GATGCTGCTGTGCTGCTCAACCTCCCTTATGCTCTGCTTGTGCTTCTTGTCCAGTTC 366
DB 301 GATGCTGCTGTGCTGCTCAACCTCCCTTATGCTCTGCTTGTGCTTCTTGTCCAGTTC 366

QY 367 ACTCACTACCGTGTCTCCAAACAGCTACTATATCCCAAGAGTCTGTGTTCACGCA 426
DB 361 ACTCACTACCGTGTCTCCAAACAGCTACTATATCCCAAGAGTCTGTGTTCACGCA 420
QY 427 GTCCTTATCTCTCACTTAACCTCTCAAGAGATGAAAGCTTCAGTGAAGTCAACC 486
DB 421 GTCCTTATCTCTCACTTAACCTCTCAAGAGATGAAAGCTTCAGTGAAGTCAACC 480
QY 487 ACCAGATGACCTCCCATCTCAACCCCACTTACAGTGAAGAGAGCCAGACTTTCAG 546
DB 481 ACCAGATGACCTCCCATCTCAACCCCACTTACAGTGAAGAGAGCCAGACTTTCAG 540
QY 547 CCGTGCCTGAGAGGCTCAAGCAACGTTGAGAGCTCTCAATCCCTGTGCTCCG 606
DB 541 CCGTGCCTGAGAGGCTCAAGCAACGTTGAGAGCTCTCAATCCCTGTGCTCCG 600
QY 607 GAGGCGCAGAGCAACGCGCAAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 666
DB 601 GAGGCGCAGAGCAACGCGCAAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 667 CCGACACAGAAACACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726
DB 661 CCGACACAGAAACACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 727 GAAAG 786
DB 721 GAAAG 780
QY 787 CAGCTGCAAG 846
DB 781 CAGCTGCAAG 840
QY 847 TCTTTTGTCCCGGGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 906
DB 841 TCTTTTGTCCCGGGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 907 GAGCTCATGATGATGAG 966
DB 901 GAGCTCATGATGATGAG 960
QY 967 TACTGAGAAACCAAAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1026
DB 961 TACTGAGAAACCAAAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1027 GTGCTGTCTATTCATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1086
DB 1021 GTGCTGTCTATTCATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1087 AAGTACATGAG 1146
DB 1081 AAGTACATGAG 1140
QY 1147 CGACATATGATCTGCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 1206
DB 1141 CGACATATGATCTGCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 1200
QY 1207 TGAAG 1266
DB 1201 TGAAG 1260
QY 1267 CCGTGTCTGCTCTGAG 1326
DB 1261 CCGTGTCTGCTCTGAG 1320
QY 1327 CCGTGTCTGAG 1386
DB 1321 CCGTGTCTGAG 1380
QY 1387 GCGACAGAAAGCTGTAAGATGTCAGAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1446
DB 1381 GCGACAGAAAGCTGTAAGATGTCAGAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440

QY 1447 TTCGAGATGGGATTTCCCTACCAAGATTGTGACACAGACTATATCCAGTACCCAAAC 1506
 DB 1441 TTCGAGATGGGATTTCCCTACCAAGATTGTGACACAGACTATATCCAGTACCCAAAC 1500
 QY 1507 TACGTTCCCTCAAGACGACAGTGTCTGATGAGAAACCCGATCCGAAGTCTCCCGC 1566
 DB 1501 TACGTTCCCTCAAGACGACAGTGTCTGATGAGAAACCCGATCCGAAGTCTCCCGC 1560
 QY 1567 ATGAGATGTCTGCAGAAATGAGACTTAACAGTGCCTGAGCCCTGGCAAAAGTGAAGACTT 1626
 DB 1561 ATGAGATGTCTGCAGAAATGAGACTTAACAGTGCCTGAGCCCTGGCAAAAGTGAAGACTT 1619
 QY 1627 GTGC-TTCGATGAGCCAGAGATTGACACTTGAAGCCAGTTCGATGAGTGG 1685
 DB 1620 GTGC-TTCGATGAGCCAGAGATTGACACTTGAAGCCAGTTCGATGAGTGG 1679
 QY 1686 CGCTATTTCCGCCCACACCCCAAGCCCACTGCTCTATGTTTGTGAGACCCC 1745
 DB 1680 SGTTATTTTGGCCACACCCCAAGCCCACTGCTCTATGTTTGTGAGACCCC 1739
 QY 1746 ATGCTTTTCAGGCTGCCCTCTGAGTCTGTACTCGGCCCTTACATTTCTGAGG 1805
 DB 1740 ATGCTTTTCAGGCTGCCCTCTGAGTCTGTACTCGGCCCTTACATTTCTGAGG 1799
 QY 1806 TTGAGACAGACAGTCCAGAGAGGCGCACGCTGAGAGCTGCCTCTTAAAGATGACT 1865
 DB 1800 TTGAGACAGACAGTCCAGAGAGGCGCACGCTGAGAGCTGCCTCTTAAAGATGACT 1859
 QY 1866 TTACATTAATGTTGATCTTCAAAAAA 1895
 DB 1860 TTACATTAATGTTGATCTTCAAAAAA 1889

RESULT 5
 AA224890
 ID AA224890 standard; DNA, 1892 BP.
 XX
 AC AA224890;
 XX
 DT 02-DEC-1999 (first entry)
 XX
 DE Human secreted protein gene 80 clone HLMV54.
 XX
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; fetal deficiency; blood; allergy; renal; ds;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; chryoiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX
 OS Homo sapiens.
 XX
 PN MO947540-A1.
 XX
 PD 23-SEP-1999.
 XX
 PF 18-MAR-1999; 99MO-US005804.
 XX
 PR 19-MAR-1998; 98US-0078563P.
 PR 19-MAR-1998; 98US-0078566P.
 PR 19-MAR-1998; 98US-0078573P.
 PR 19-MAR-1998; 98US-0078574P.
 PR 19-MAR-1998; 98US-0078576P.
 PR 19-MAR-1998; 98US-0078577P.
 PR 19-MAR-1998; 98US-0078578P.
 PR 19-MAR-1998; 98US-0078579P.
 PR 19-MAR-1998; 98US-0078581P.
 PR 01-APR-1998; 98US-0080312P.
 PR 01-APR-1998; 98US-0080313P.
 PR 01-APR-1998; 98US-0080314P.
 XX

PA (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM, Ni J, Rosen CA, Yu G, Young PE, Feng P, Soppet DR;
 PI Wei Y, Endress GA, Duan RD, Kyaw H, Ebner R, Latleur DW, Olsen HS;
 PI Shi Y, Moore PA.
 XX WPI; 1999-562050/47.
 DR P-PSDB; AAY41387.
 XX
 PT New isolated human genes, useful for diagnosis and treatment of e.g.
 PT cancers, neurological disorders, immune diseases, inflammation or blood
 PT disorders.
 XX
 PS
 PS
 XX
 XX
 CC This sequence represents a nucleic acid molecule which encodes a secreted
 CC human protein. The gene number, and the clone it is derived from, are
 CC detailed in the descriptor line. The gene can be used to generate fusion
 CC proteins by linking to the gene to a human immunoglobulin Fc portion
 CC (e.g. AA224802) for increasing the stability of the fused protein as
 CC compared to the human protein only. The invention relates to 95 novel
 CC genes and their fragments (nucleic acid sequences: AA224811-224907; amino
 CC acid sequences AA141308-141404) which are useful for preventing, treating
 CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,
 CC pathological conditions can be diagnosed by determining the amount of the
 CC new polypeptides in a sample or by determining the presence of mutations
 CC in the new polynucleotides. Specific uses are described for each of the
 CC 95 polynucleotides, based on which tissues they are most highly expressed
 CC in (see AA224811 for described uses)
 XX
 SQ Sequence 1892 BP; 461 A; 565 C; 472 G; 394 T; 0 U; 0 Other;

Query Match 95.6%; Score 1811.2; DB 2; Length 1892;

Best Local Similarity 99.4%; Pred. No. 0; Matches 1860; Conservative 0; Mismatches 8; Indels 4; Gaps 4;

QY 24 GGAAGCGGGGAGATCTTCTCCGCGCATGAGAGAGCCAGCTGCTCTTCCCTCACT 83
 DB 13 GGAAGCGGGGAGATCTTCTCCGCGCATGAGAGAGCCAGCTGCTCTTCCCTCACT 72
 QY 84 CTTGAAGTGTCTGCTCTGCTCTGCGCACTGCGCAGCCAGAGATTGACTAGGCC 143
 DB 73 CTTGAAGTGTCTGCTCTGCTCTGCGCACTGCGCAGCCAGAGATTGACTAGGCC 132
 QY 144 CACTCCAGAGAGCCCTCTCTCTACCGAATGGAAGCGCTTCTGCGACTGCTGCTCC 203
 DB 133 CACTCCAGAGAGCCCTCTCTCTACCGAATGGAAGCGCTTCTGCGACTGCTGCTCC 192
 QY 204 AACCTGGAAGGACAGACTACTGCTGCTGCGTCAACCCAGCGCTGCGGAATCCAC 263
 DB 193 AACCTGGAAGGACAGACTACTGCTGCTGCGTCAACCCAGCGCTGCGGAATCCAC 252
 QY 264 ACTGTCAGCTGAGACCAATATGAAAAACAGCGCTTAGTCCCGAGTGTCTGCTC 323
 DB 253 ACTGTCAGCTGAGACCAATATGAAAAACAGCGCTTAGTCCCGAGTGTCTGCTC 312
 QY 324 CAACCTCCCTTATGCTCCCTGCTTGTGAGTCTTCTGCGCACTTCACTACACGTTGCTC 383
 DB 313 CAACCTCCCTTATGCTCCCTGCTTGTGAGTCTTCTGCGCACTTCACTACACGTTGCTC 372
 QY 384 CAACCAAGTCTATGAGCCAGAGAGCTGTGTTCCAGCCAGTCTTATCTCTGACC 443
 DB 373 CAACCAAGTCTATGAGCCAGAGAGCTGTGTTCCAGCCAGTCTTATCTCTGACC 432
 QY 444 TAAACCTCTCAAGAGATGAGAGCTTCACTGAAGTCTCAACCAAGATGACTCTCC 503
 DB 433 TAAACCTCTCAAGAGATGAGAGCTTCACTGAAGTCTCAACCAAGATGACTCTCC 492
 QY 504 CATCTACCCCACTTCAAGTGAAGAGCGCAGACCTTCAAGCCCTGAGTGAAGGCT 563
 DB 493 CATCTACCCCACTTCAAGTGAAGAGCGCAGACCTTCAAGCCCTGAGTGAAGGCT 552
 QY 564 CAGCAACAGTGAAGAGCTCTTACAGATCTCTTGTCCCTGAGAGCGCAGAGCAAGC 623

Db 553 CAGCAACACGAGGAGAGCTCTTCACTCTCTTGTCCCTGGAAACCCAGGAGCAGC 612
 Qy 624 GGCAGAGCAACAGCAGAGGACAAAGAGTGAGACACAGGAGAGGCCGACACAAGAACCA 683
 Db 613 GCGAGAGCAACAGCAGAGGACAAAGAGTGAGACACAGGAGAGGCCGACACAAGAACCA 672
 Qy 684 GCAGAGAGAGGGGACAAACAGAGAGACAAAGAGAGAAACAGAGAGAGAGAGAGAGAG 743
 Db 673 GCAGAGAGAGGGGACAAACAGAGAGACAAAGAGAGAAACAGAGAGAGAGAGAGAG 742
 Qy 744 GGAAG 803
 Db 733 GGAAG 792
 Qy 804 AGAGCCCAAGTTTCACTGAACTCTATCTCTTCAACCCCTCTCTCTCTCTCTCTCTCT 863
 Db 793 AGAGCCCAAGTTTCACTGAACTCTATCTCTTCAACCCCTCTCTCTCTCTCTCTCTCT 852
 Qy 864 ACGAAG 923
 Db 853 ACGAAG 912
 Qy 924 CAGAGAAATAGATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 983
 Db 913 CAGAGAAATAGATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 972
 Qy 984 CCGTGGAGAGCTTCTGAGAGCTGCCCAACAGAGAGCTTGTGAGCTGTGATTTGAT 1043
 Db 973 CCGTGGAGAGCTTCTGAGAGCTGCCCAACAGAGAGCTTGTGAGCTGTGATTTGAT 1031
 Qy 1044 CGTGAGAAATACCTGATCATTAACCCCAACAGAGAGCTTGTGAGCTGTGATTTGAT 1103
 Db 1032 CGTGAGAAATACCTGATCATTAACCCCAACAGAGAGCTTGTGAGCTGTGATTTGAT 1091
 Qy 1104 GATCCTGTGTTTGGGAGAGTCCGCTGTGAGACCTTGTGAGAGCTTGTGAGAGAG 1163
 Db 1092 GATCCTGTGTTTGGGAGAGTCCGCTGTGAGACCTTGTGAGAGCTTGTGAGAGAG 1151
 Qy 1164 TGCCCTGTGAGCTTCTGATCTCTTGAAGTGAGAGAGCTTGTGAGAGAGCTTGTGAG 1223
 Db 1152 TGCCCTGTGAGCTTCTGATCTCTTGAAGTGAGAGAGCTTGTGAGAGAGCTTGTGAG 1211
 Qy 1224 GGGGCAACATGCGACACCTCCCAACAGAGCTTGTGAGAGAGCTTGTGAGAGAGCTTGTG 1283
 Db 1212 GGGGCAACATGCGACACCTCCCAACAGAGCTTGTGAGAGAGCTTGTGAGAGAGCTTGTG 1270
 Qy 1284 GAGCTGTGATCGGCAACAG 1343
 Db 1271 GAGCTGTGATCGGCAACAG 1330
 Qy 1344 TTTGTAAGTGGGCTCCACATGAGCTTCTGAGTGGCCGGCTTGTGAGAGAGAGAGAG 1403
 Db 1331 TTTGTAAGTGGGCTCCACATGAGCTTCTGAGTGGCCGGCTTGTGAGAGAGAGAGAG 1390
 Qy 1404 AGATGTCCGAGCTCTGAGTGGGCTCCACATGAGCTTCTGAGTGGGCTTGTGAGAGAG 1463
 Db 1391 AGATGTCCGAGCTCTGAGTGGGCTCCACATGAGCTTCTGAGTGGGCTTGTGAGAGAG 1449
 Qy 1464 CCGTACCAAGTTTGTGACACAGACTATCCAGTCCCAAACTACTGTTCTCTCAAAAG 1523
 Db 1450 CCGTACCAAGTTTGTGACACAGACTATCCAGTCCCAAACTACTGTTCTCTCAAAAG 1509
 Qy 1524 CAGAGAGAGCTGATGAG 1583
 Db 1510 CAGAGAGAGCTGATGAG 1569
 Qy 1584 TGAAGCTTACAGTGGCTGAGCCCTGCAAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 1643
 Db 1570 TGAAGCTTACAGTGGCTGAGCCCTGCAAAAGTGAAGAGAGAGAGAGAGAGAGAGAG 1629
 Qy 1644 GGAGTTCAGAGACCTTACCTTGAAGCCAGTTGGAGTGAAGCTTATCTTGTGCGCACAC 1703

Db 1630 GGAAGTTCAGACCTTGACTTGAAGCCAGTTCCGATGAGAGTGGCGTCTATTCTGCCACAC 1689
 Qy 1704 CCGAGCCCAACCTGCGCCAGCTTCTATTGTTTGAAGCCCAATGCTTTTCAAGCTGCC 1763
 Db 1690 CCGAGCCCAACCTGCGCCAGCTTCTATTGTTTGAAGCCCAATGCTTTTCAAGCTGCC 1749
 Qy 1764 CTTTGGGCTCTGTTACCTCGGCTTCTACTCAATTTCTTGGGTTGAGAGACAGTCCAG 1823
 Db 1750 CTTTGGGCTCTGTTACCTCGGCTTCTACTCAATTTCTTGGGTTGAGAGACAGTCCAG 1809
 Qy 1824 AGAGGGCCACGTTGGAGAGTGGCCCTCTTAAAGATGACTTAAATTAATTTGATC 1883
 Db 1810 AGAGGGCCACGTTGGAGAG-TGCCCTCTCTTAAAGATGACTTAAATTAATTTGATC 1868
 Qy 1884 TTCAAAAAAAA 1895
 Db 1869 TTCAAAAAAAA 1880

RESULT 6
 ID AD39940 standard; cDNA, 1892 BP.
 AD39940

AC AD39940;
 XX

DT 20-NOV-2003 (first entry)
 XX

DE Human secreted protein encoding cDNA.
 XX

KW Human; secreted protein; cancer; hyperproliferative disorder;
 KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
 KW anaemia; allergic reaction; asthma; cardiovascular disorder;
 KW wound healing; cytoskeletal; immunosuppressive; neurotropic; neuroprotective;
 KW antiviral; anticancer; hepatocellular; antidiabetic; antiinflammatory;
 KW vulnery; cardiac; gene therapy; ss.
 OS

XX Homo sapiens.
 PN

MO2002102993-A2.
 PD

XX 27-DEC-2002.
 XX

PF 19-MAR-2002; 2002WO-US008123.
 XX

PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-031287P.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX

PI Rosen CA, Ruben SM,
 XX

DR WPI; 2003-175238/17.
 XX

PT New human secreted proteins and nucleic acid molecules, useful for
 PT preparing a diagnostic or pharmaceutical composition for
 PT preventing or treating cancer or other hyperproliferative disorder,
 PT asthma, allergies or AIDS.
 PS

XX Claim 9; SEQ ID NO 322; 3205bp; English.
 PS

CC The invention relates to novel genes AD39629-AD40565 and proteins
 CC AD39629-AD40565 for human secreted proteins, useful for preventing,
 CC treating or ameliorating medical conditions e.g. by protein or gene
 CC therapy. The polypeptides, nucleic acid molecules, antibodies or gene
 CC fragments, and agonists or antagonists that bind to the polypeptide are
 CC useful for preparing a diagnostic or pharmaceutical composition for
 CC diagnosing or treating cancer or other hyperproliferative disorder. The
 CC polypeptides and nucleic acid molecules are also useful for detecting,
 CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
 CC or other hyperproliferative disorders including neoplasms, autoimmune
 CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
 CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic

CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
CC thrombocytopenia), allergic reactions including asthma or eczema,
CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
CC fungal or viral infections including HIV/AIDS), or wound healing and
CC disorders of epithelial cell proliferation. The nucleic acids are also
CC useful for chromosome identification, radiation hybrid mapping or long-
CC range restriction mapping, as molecular weight markers, or as
CC hybridization or diagnostic probes. The polypeptides and antibodies are
CC useful for providing immunohistochemical probes for differential identification
CC of the tissues immunohistochemistry assays. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1892 BP; 461 A; 565 C; 472 G; 394 T; 0 U; 0 Other;

Query Match 95.6%; Score 1811.2; DB 8; Length 1892;

Best Local Similarity 99.4%; Pred. No. 0;
Matches 1860; Conservative 0; Mismatches 8; Indels 4; Gaps 4;

QY 24 GGAAGCGGGGCGATCTTCTCCGCGCATGAGGAAGCCAGCGCTGCTTCTTCTCCCTCACT 83
DB 13 GGAAGCGGGGCGATCTTCTCCGCGCATGAGGAAGCCAGCGCTGCTTCTTCTCCCTCACT 72
QY 84 CCGAAGGCTGCTCTCTGCTCTGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 143
DB 73 CCGAAGGCTGCTCTCTGCTCTGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 132
QY 144 CACTCCAGGAGCGCT 203
DB 133 CACTCCAGGAGCGCT 192
QY 204 AACCTGGAAGGAG 263
DB 193 AACCTGGAAGGAG 252
QY 264 ACTCGTCAGCTGAG 323
DB 253 ACTCGTCAGCTGAG 312
QY 324 CAACCTCCCTTATGCT 383
DB 313 CAACCTCCCTTATGCT 372
QY 384 CAACCACTCTATGAG 443
DB 373 CAACCACTCTATGAG 432
QY 444 TAAACATCTTCAG 503
DB 433 TAAACATCTTCAG 492
QY 504 CATCTCACTCCATCTTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 563
DB 493 CATCTCACTCCATCTTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 552
QY 564 CAGCAACAACTGGAAG 623
DB 553 CAGCAACAACTGGAAG 612
QY 624 GCCAGAGCAAG 683
DB 613 GCCAGAGCAAG 672
QY 684 GCAGGAAG 743
DB 673 GCAGGAAG 732
QY 744 GGAAG 803

DB 733 GGAAG 792
QY 804 AGAGCCCAAGTTTCACTGATGATCTATCTTAAACCTTCTCTTTTCTCTCCCGGGT 863
DB 793 AGAGCCCAAGTTTCACTGATGATCTATCTTAAACCTTCTCTTTTCTCTCCCGGGT 852
QY 864 ACAGAGAGTGAAGTCTACTCTATGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 923
DB 853 ACAGAGAGTGAAGTCTACTCTATGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 912
QY 924 CCAGGAATATGATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 983
DB 913 CCAGGAATATGATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 972
QY 984 CCTGAGAGCTTCTGAGAGTGGCCCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1043
DB 973 CCTGAGAGCTTCTGAGAGTGGCCCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1031
QY 1044 CCGTGAAGATACCTGATCATTAACCCCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1103
DB 1032 CCGTGAAGATACCTGATCATTAACCCCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1091
QY 1104 GATCTTGGTTTGGGAGAGTGGTCTGTGACAGCTTTGGGCGGCGACATGCTTACTG 1163
DB 1092 GATCTTGGTTTGGGAGAGTGGTCTGTGACAGCTTTGGGCGGCGACATGCTTACTG 1151
QY 1164 TGCCCTCTGATCTTGTGCTCTTGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1223
DB 1152 TGCCCTCTGATCTTGTGCTCTTGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1211
QY 1224 GCGGCAACATGAG 1283
DB 1212 GCGGCAACATGAG 1270
QY 1284 GAGCTGTTCATGAG 1343
DB 1271 GAGCTGTTCATGAG 1330
QY 1344 TTGTGAG 1403
DB 1331 TTGTGAG 1390
QY 1404 AGATGTCCAGAGTCTCGGGTGGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1463
DB 1391 AGATGTCCAGAGTCTCGGGTGGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1449
QY 1464 CCTTCAAGATTTGAG 1523
DB 1450 CCTTCAAGATTTGAG 1509
QY 1524 CCAAGAGTGTGATGAG 1583
DB 1510 CCAAGAGTGTGATGAG 1569
QY 1584 TGAAGCTTACAGTGCCTGAG 1643
DB 1570 TGAAGCTTACAGTGCCTGAG 1629
QY 1644 GGAAGTTCAGACCTTGAAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1703
DB 1630 GGAAGTTCAGACCTTGAAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1689
QY 1704 CCGAGCCCAACCTGAG 1763
DB 1690 CCGAGCCCAACCTGAG 1749
QY 1764 CTTCTGGGTCTGTACTCTGAG 1823
DB 1750 CTTCTGGGTCTGTACTCTGAG 1809
QY 1824 AGAGGGGCAAGGTGGAG 1883
DB 1810 AGAGGGGCAAGGTGGAG 1868

Db 1032 CGTGAGAAATCTGCATCAATACCCCAAGCCCTGGAATGATGAGAGGA 1091
 QY 1104 GATCCTTGTGTTGGGAAAGTGGTGTGTGACAGCTTGGGGGAGACATGTCTACTG 1163
 Db 1092 GATCCTTGTGTTGGGAAAGTGGTGTGTGACAGCTTGGGGGAGACATGTCTACTG 1151
 QY 1164 TGGCTCTGTGACTTGTCTCTTGAAGGTGAGACAGTGCCTCAGAGGCCAGCTGCA 1223
 Db 1152 TGGCTCTGTGACTTGTCTCTTGAAGGTGAGACAGTGCCTCAGAGGCCAGCTGCA 1211
 QY 1224 GGGGCAACAATGAGCACTCCCAACAAGATCCCTTTGTAGAGCCCTTGTGCTTCCA 1283
 Db 1212 GGGGCAACAATGAGCACTCCCAACAAGATCCCTTTGTAGAGCCCTTGTGCTTCCA 1270
 QY 1284 GAGCTGTCCATGAGCAACAGGATAGGATCCCAAGATCAGGCGCTTTACGGGCTGGA 1343
 Db 1271 GAGCTGTCCATGAGCAACAGGATAGGATCCCAAGATCAGGCGCTTTACGGGCTGGA 1330
 QY 1344 TTTGTACGTTGGGCTCCACATGAGACTTCTGTGTGCTCCGCTTTGCCACGAAAGCTGTGA 1403
 Db 1331 TTTGTACGTTGGGCTCCACATGAGACTTCTGTGTGCTCCGCTTTGCCACGAAAGCTGTGA 1390
 QY 1404 AGATGTCGAGTCTCTGGGTGGTCTCCAGACTGAGTCTTACGTTCCAGATGGGATTT 1463
 Db 1391 AGATGTCGAGTCTCTGGGTGGTCTCCAGACTGAGTCTTACGTTCCAGATGGGATTT 1449
 QY 1464 CCTTACCAAGATTTTGAACAGACTATATCCAGTACCCAACTACTGTTCTTCAAAAG 1523
 Db 1450 CCTTACCAAGATTTTGAACAGACTATATCCAGTACCCAACTACTGTTCTTCAAAAG 1509
 QY 1524 CCAGCAGTGTCTGATGAGAAACCGCAATCGAAAGTGTCCGATGAGATGTCTGCAGAA 1583
 Db 1510 CCAGCAGTGTCTGATGAGAAACCGCAATCGAAAGTGTCCGATGAGATGTCTGCAGAA 1569
 QY 1584 TGAAGATTACAGTGGCTGTGAGCCCTTGGCAAAAGTGAAGAGTGTGTGATGAGAGCCA 1643
 Db 1570 TGAAGATTACAGTGGCTGTGAGCCCTTGGCAAAAGTGAAGAGTGTGTGATGAGAGCCA 1629
 QY 1644 GAGATTACAGCTTACTCTAGAGCAAGTTCGAGATGAGTGGGCTTATCTGCCCCAC 1703
 Db 1630 GAGATTACAGCTTACTCTAGAGCAAGTTCGAGATGAGTGGGCTTATCTGCCCCAC 1689
 QY 1704 CCCAGGCCAAGCTGCCACAGTTCATATGTTTGAAGACCCCAATGCTTCAAGCTGCC 1763
 Db 1690 CCCAGGCCAAGCTGCCACAGTTCATATGTTTGAAGACCCCAATGCTTCAAGCTGCC 1749
 QY 1764 CTCTGGGTCTGTACTCGGCCCCCTTACTACATTTCTTGGGTTGAAGCAAGTCCAG 1823
 Db 1750 CTCTGGGTCTGTACTCGGCCCCCTTACTACATTTCTTGGGTTGAAGCAAGTCCAG 1809
 QY 1824 AGAGGGCCACGAGTGGAGCTGGCCCTTAAAGATGACTTACATTAATGTTGATC 1883
 Db 1810 AGAGGGCCACGAGTGGAG-TCGCGCCCTCTTAAGATGACTTACATTAATGTTGATC 1868
 QY 1884 TTCAAAAAAA 1895
 Db 1869 TTCAAAAAAA 1880
 RESULT 8
 ADD37623
 ID ADD37623 standard; cDNA; 1892 BP.
 XX
 AC ADD37623;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human secreted protein encoding sequence #105.
 XX
 KW human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;
 XX Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic; ss.
 OS Homo sapiens.

XX MO200290526-A2.
 PN 14-NOV-2002.
 XX
 PD 19-MAR-2002; 2002MO-US008279.
 XX
 PF 21-MAR-2001; 2001US-0277340P.
 XX
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2003-140218/13.
 XX
 XX
 PT New human secreted proteins and nucleic acid molecules, useful for
 PT preparing a diagnostic or pharmaceutical composition for diagnosing or
 PT treating allergic or asthmatic disorders, or related immediate
 PT hypersensitivity disorders.
 PT
 PS Claim 7; SEQ ID NO 105; 1323bp; English.
 XX
 CC The present invention relates to an isolated polypeptide or human
 CC secreted protein. The polypeptides, nucleic acid molecules, antibodies or
 CC their fragments, and agonists or antagonists that bind are useful for
 CC preparing a diagnostic or pharmaceutical composition for diagnosing or
 CC treating allergic or asthmatic disorders. The polypeptide is also useful
 CC for identifying a binding partner by contacting the polypeptide with a
 CC binding partner, and determining whether the binding partner increases or
 CC decreases the activity of the polypeptide. The polypeptides and nucleic
 CC acid molecules are also useful for detecting, preventing, diagnosing,
 CC prognosticating, treating or ameliorating inflammatory disorders
 CC neoplastic diseases, wound healing and disorders of epithelial cell
 CC proliferation, immune disorders, cardiovascular disorders, blood-related
 CC disorders, infectious diseases, endocrine disorders, or gastrointestinal
 CC disorders. The nucleic acids are also useful for chromosome
 CC identification, radiation hybrid mapping or long-range restriction
 CC mapping, as molecular weight markers, or as hybridization or diagnostic
 CC probes. The polypeptides and antibodies are useful for providing
 CC immunological probes for differential identification of the tissues
 CC immunohistochemistry assays. The present sequence represents a human
 CC secreted protein encoding sequence.
 CC
 SQ Sequence 1892 BP; 461 A; 565 C; 472 G; 394 T; 0 U; 0 Other;
 Query Match 95.6%; Score 1811.2; DB 10; Length 1892;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1860; Conservative 0; Mismatches 8; Indels 4; Gaps 4;
 QY 24 GAGAGGGGGGAGATCTTCTCCGGCCATGAGAGAGCCAGCCGCTTCTTCCCTCACT 83
 Db 13 GGGAGCCGAGAGATCTTCTCCGGCCATGAGAGAGCCAGCCGCTTCTTCCCTCACT 72
 QY 84 CCTGAAGTGTCTCTCTGCTGTGACCTGGCCGAGCCAGATTCAGTCAAGGCC 143
 Db 73 CCTGAAGTGTCTCTCTGCTGTGACCTGGCCGAGCCAGATTCAGTCAAGGCC 132
 QY 144 CACTCCAGGAGCCCTCTCTCTCTTACCGAATACGAACCTTCTTGAAGTGTGACTGC 203
 Db 133 CACTCCAGGAGCCCTCTCTCTCTTACCGAATACGAACCTTCTTGAAGTGTGACTGC 192
 QY 204 AACCTGGAAGGAGAGACTACTGCGCTTCCGTGCAACCCAGCGTCCCGGAATCCAC 263
 Db 193 AACCTGGAAGGAGAGACTACTGCGCTTCCGTGCAACCCAGCGTCCCGGAATCCAC 252
 QY 264 ACTCGTCAGCTGAGCAATATGAAAAACAGAGGCTTAGGCCGATGAGTGTGTGCTC 323
 Db 253 ACTCGTCAGCTGAGCAATATGAAAAACAGAGGCTTAGGCCGATGAGTGTGTGCTC 312
 QY 324 CAACTCCCTTATGCTCTGTGTTGAGTCTTTTCTGCAAGTTCACACTACCGTTGCTC 383

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Db      313 CAACCTCCCTTATGCTCCCTGCTTGAAGTCTTTCTGCGCAATTCATCACTACCGTGTCTC 372
Qy      384 CAACCAAGTCTATATGCGCAAGAGATCTGTGTCTCCAGCGCACTCTATTTCTCTACC 443
Db      373 CAACCAAGTCTATATGCGCAAGAGATCTGTGTCTCCAGCGCACTCTATTTCTCTACC 443
Qy      444 TAACTCTCAAGAGATGAAAGCTTCACTGAAAGTCTCAACCAACATGACTCTCC 432
Db      433 TAACTCTCAAGAGATGAAAGCTTCACTGAAAGTCTCAACCAACATGACTCTCC 432
Qy      504 CATCTCAACCCCACTTCAAGTGAAGCAAGCCCAAGCTTCCAGCCCTGAGCTGAAAGCT 563
Db      493 CATCTCAACCCCACTTCAAGTGAAGCAAGCCCAAGCTTCCAGCCCTGAGCTGAAAGCT 552
Qy      564 CAGCAACAACGTGGAAGAGCTCTCAATCTCTCTGTCTCTGGAAGCCCAAGCAAGCT 623
Db      553 CAGCAACAACGTGGAAGAGCTCTCAATCTCTCTGTCTCTGGAAGCCCAAGCAAGCT 612
Qy      624 GCCAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 672
Db      613 GCCAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 672
Qy      684 GCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 743
Db      673 GCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 732
Qy      744 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 803
Db      733 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 792
Qy      804 AGAGCCCAAGTTTCACTGAACTCTATCTTCTTAACTCTCTCTCTCTCTCTCTCTCT 863
Db      793 AGAGCCCAAGTTTCACTGAACTCTATCTTCTTAACTCTCTCTCTCTCTCTCTCTCT 852
Qy      864 ACGAGAGATAGAGTCTACTCTATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 923
Db      853 ACGAGAGATAGAGTCTACTCTATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 912
Qy      924 CCAGAGATAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 983
Db      913 CCAGAGATAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 972
Qy      984 CCCGAGAGAGTCTCTCAAGCTGCCCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1043
Db      973 CCCGAGAGAGTCTCTCAAGCTGCCCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1031
Qy      1044 CGTGAAGATACCTGATATATATATATATATATATATATATATATATATATATAT 1103
Db      1032 CGTGAAGATATCTGATATATATATATATATATATATATATATATATATATATAT 1091
Qy      1104 GATCTTGTGTTCCGGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1163
Db      1092 GATCTTGTGTTCCGGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1151
Qy      1164 TGCCTCTGTGATCTTGTCTCTTGAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1223
Db      1152 TGCCTCTGTGATCTTGTCTCTTGAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1211
Qy      1224 GCGGCAACAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1283
Db      1212 GCGGCAACAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1270
Qy      1284 GAGCTGTCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1343
Db      1271 GAGCTGTCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1330
Qy      1344 TTTGTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1403
Db      1331 TTTGTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1390
Qy      1404 AGATGTCAGAGTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1463
Db      1391 AGATGTCAGAGTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1449

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Qy      1464 CCTTCAAGATTTGTGACACAGACTATATCTCACTATCCCAACTACTGTCTTCAAAAG 1523
Db      1450 CCTTCAAGATTTGTGACACAGACTATATCTCACTATCCCAACTACTGTCTTCAAAAG 1509
Qy      1524 CCAGAGAGTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1583
Db      1510 CCAGAGAGTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1569
Qy      1584 TGAAGCTTACAGTCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1643
Db      1570 TGAAGCTTACAGTCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1629
Qy      1644 GGAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1703
Db      1630 GGAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1689
Qy      1704 CCCAGCCCAACTGCCCCAGTCTCTATGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1763
Db      1690 CCCAGCCCAACTGCCCCAGTCTCTATGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1749
Qy      1764 CTCTGAGTCTGTTACTGAGCCCTTACTACATTTCTTGTGAGAGAGAGAGAGAGAGAG 1823
Db      1750 CTCTGAGTCTGTTACTGAGCCCTTACTACATTTCTTGTGAGAGAGAGAGAGAGAGAG 1809
Qy      1824 AGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1883
Db      1810 AGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1868
Qy      1884 TTTCAAAAAA 1895
Db      1869 TTTCAAAAAA 1880

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RESULT 9
ADA56130
ID      ADA56130 standard; DNA; 1892 BP.
XX      AC      ADA56130;
XX      DT      20-NOV-2003 (first entry)
DE      XX      Gene encoding human secreted protein #309.
KW      KW      immunosuppressive; antiinflammatory; antiaesthetic; antiallergic;
KW      KW      cytoskeletal; cerebroprotective; neuroprotective; neurotropic;
KW      KW      cardiovascular; antihypertensive; antihypertensive; antihypertensive;
KW      KW      human secreted protein; immune disorder; inflammation;
KW      KW      inflammatory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW      KW      multiple sclerosis; ischemic brain injury; Parkinson's disease;
KW      KW      Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW      KW      triple helix formation; antisense gene therapy; forensic biology; ds;
XX      OS      Homo sapiens.
XX      PN      MO2002102994-A2.
XX      PD      27-DEC-2002.
XX      PF      19-MAR-2002; 2002MO-US008278.
XX      PR      21-MAR-2001; 2001US-0277340P.
XX      PR      19-JUL-2001; 2001US-0306171P.
XX      PR      13-NOV-2001; 2001US-0331287P.
XX      PA      (HUMA-) HUMAN GENOME SCI INC.
XX      PI      Rosen CA, Ruben SM;
XX      WI      MPI; 2003-167512/16.
XX      DR      P-PSDB; ADA57026.

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XX New human secreted polypeptides and polynucleotides, useful for
 PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
 PT conditions, respiratory disorders, cancers, CNS disorders, or
 PT neurodegenerative disorders.

PS Claim 21; SEQ ID NO 319; 1754bp; English.

XX The invention relates to 592 new human secreted polypeptides useful for
 CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
 CC conditions, respiratory disorders, cancers, CNS disorders, or
 CC neurodegenerative disorders, or polypeptides comprising an amino acid
 CC sequence at least 95% identical to the new sequences. The polypeptides,
 CC antibodies or antibody fragments that bind to the polypeptides, nucleic
 CC acids encoding the polypeptides, agonists or antagonists that binds to
 CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
 CC compositions for diagnosing, treating or preventing an e.g. immune
 CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
 CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
 CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
 CC (e.g. multiple sclerosis or ischemic brain injury), neurodegenerative
 CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
 CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
 CC polynucleotides are useful for chromosome identification, chromosome
 CC mapping, for controlling gene expression through triple helix formation
 CC or antisense DNA or RNA, in gene therapy, for identifying individuals
 CC from minute biological samples, in forensic biology, and as hybridization
 CC probes. The polypeptides are useful for as molecular weight markers on
 CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
 CC gels, to raise antibodies, for testing biological activities, and for
 CC treating or preventing neural disorders, immune system disorders,
 CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
 CC renal, proliferative and/or cancerous diseases. This sequence corresponds
 CC to a gene encoding one of the polypeptide of the invention. Note: The
 CC sequence data for this patent did form part of the printed specification,
 CC but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 1892 BP; 461 A; 565 C; 472 G; 394 T; 0 U; 0 Other;

XX Query Match 95.6%; Score 1811.2; DB 10; Length 1892;

XX Best Local Similarity 99.4%; Pred. No. 0;

XX Matches 1860; Conservative 0; Mismatches 8; Indels 4; Gaps 4;

XX 24 GAGACGGGGCGGATCTTCTCCGSCATGAGAGAGCCAGCGTGGCTTCTCCCTACT 83
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 XX 13 GGGACCGGAGCGATCTTCTCCGSCATGAGAGAGCCAGCGTGGCTTCTCCCTACT 72
 XX |||||
 XX 84 CCTGAAGGTGCTGCTCTGCTTGGCACTGCGGAGCCAGATTGCACTGAGCCCC 143
 XX |||||
 XX 73 CCTGAAGGTGCTGCTCTGCTTGGCACTGCGGAGCCAGATTGCACTGAGCCCTC 132
 XX |||||
 XX 144 CACTCCAGGAGCGCTCTCTCTTACCGAATACGAACGTTTGGCACTGCTGACTCC 203
 XX |||||
 XX 133 CACTCCAGGAGCGCTCTCTCTTACCGAATACGAACGTTTGGCACTGCTGACTCC 192
 XX |||||
 XX 204 AACCTTGAAGGAGAGACTACCTGCGCTCCGATGCAACCGAGGTCGCGGAATCCAC 253
 XX |||||
 XX 193 AACCTTGAAGGAGAGACTACCTGCGCTCCGATGCAACCGAGGTCGCGGAATCCAC 252
 XX |||||
 XX 264 ACTCGTCAGCTGAGCAATATGAAAAACAAGGCTTAGTGCCGATGAGTGTGCTC 323
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 XX 253 ACTCGTCAGCTGAGCAATATGAAAAACAAGGCTTAGTGCCGATGAGTGTGCTC 312
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 XX 324 CAACCTCCCTTATGCTCTGCTGTTTGAAGTCTTCTGCACTTCACTACCGTTGCTC 383
 XX |||||
 XX 313 CAACCTCCCTTATGCTCTGCTGTTTGAAGTCTTCTGCACTTCACTACCGTTGCTC 372
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 XX 384 CAACCACTCTATATGAGAGAGTCTGTGTTCCAGCCAGTCTTATCTCTACCC 443
 XX |||||
 XX 373 CAACCACTCTATATGAGAGAGTCTGTGTTCCAGCCAGTCTTATCTCTACCC 442
 XX |||||
 XX 444 TAACTCTCTAAGGAGATGAAAGCTTCACTGAAGTCTCAACCAACGATGACTCCCC 503

DB 433 TAACTCTCTAAGGAGATGAAAGCTTCACTGAAGTCTCAACCAACGATGACTCCCC 492
 DB |||||
 DB 504 CATCTCAACCCCACTTCACTGAGTACAGAAAGCAGACCTTCAGGCTGGCTGAGAGCT 563
 DB |||||
 DB 493 CATCTCAACCCCACTTCACTGAGTACAGAAAGCAGACCTTCAGGCTGGCTGAGAGCT 552
 DB |||||
 DB 564 CAGCAACCACTGAGGAGAGCTCTTACATCTCTTGTCTCCCTGGAGCCAGAGCAAGC 623
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 DB 553 CAGCAACCACTGAGGAGAGCTCTTACATCTCTTGTCTCCCTGGAGCCAGAGCAAGC 612
 DB |||||
 DB 624 GCCAGAGCAACAGAGAGAGAGAGTGGAGCAACAGGAGAGCCAGCAACAGACAA 683
 DB |||||
 DB 613 GCCAGAGCAACAGAGAGAGAGAGTGGAGCAACAGGAGAGCCAGCAACAGACAA 672
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 DB 684 GCAGGAAGAGGGGACGAAACAGGAAGGCAAGGAAGGAACAGGAAGAGGAAAGCA 743
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 DB 673 GCAGGAAGAGGGGACGAAACAGGAAGGCAAGGAAGGAACAGGAAGAGGAAAGCA 732
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 DB 744 GGAAGGAAGGACAGGGGACTAAGAGAGGACGGAGGCTGTCTCAGCTGCACAGACTC 803
 DB |||||
 DB 733 GGAAGGAAGGACAGGGGACTAAGAGAGGACGGAGGCTGTCTCAGCTGCACAGACTC 792
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 DB 793 AGAGCCCAAGTTTCACTTGAATCTCTATCTTAACTCTTCTTTGCTCCCGGGT 852
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 DB |||||
 DB 853 ACAGGAAGTGAATCTTACTCTCTATCTTGAATAGGAACATCCAGAGCTCATTTGATACG 912
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 DB 924 CCAGGAATATGATGAATGAATGAATATATATATGAGAACTCTTACCTGAGAAACCAAA 983
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 DB 913 CCAGGAATATGATGAATGAATGAATATATATATGAGAACTCTTACCTGAGAAACCAAA 972
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 DB 973 CCCTGGCAGCTTCTCTGCAAGTGGCCCAACAGAGGCTTGTGTGTGTGTAATGAT 1031
 DB |||||
 DB 1044 CCGTGAAGTATCTGATCATTAACCCCAACAGGAGCCCTGGAATGATGAGAGAGGA 1103
 DB |||||
 DB 1032 CCGTGAAGTATCTGATCATTAACCCCAACAGGAGCCCTGGAATGATGAGAGAGGA 1091
 DB |||||
 DB 1104 GATCTTGTGTTTGGGAAAGTGGCTGTGTGACAGCTTGGGCGGAGCAACATGTCTACTG 1163
 DB |||||
 DB 1092 GATCTTGTGTTTGGGAAAGTGGCTGTGTGACAGCTTGGGCGGAGCAACATGTCTACTG 1151
 DB |||||
 DB 1164 TGCCTCTGTGACTTGTCTCTTGAAGCTGAGCAAGTCACTCAAGGCGAGCTTGCA 1223
 DB |||||
 DB 1152 TGCCTCTGTGACTTGTCTCTTGAAGCTGAGCAAGTCACTCAAGGCGAGCTTGCA 1211
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 DB 1224 GCGGCAACATGAGCAACCTCCCAAGAACTCCCTTGTGACGCCCTTGTGCTGCCA 1283
 DB |||||
 DB 1212 GCGGCAACATGAGCAACCTCCCAAGAACTCCCTTGTGACGCCCTTGTGCTGCCA 1270
 DB |||||
 DB 1284 GAGCTGTGCATGAGCAACAGGTAGAGTCCCAAGATCAGAGCGGCTTTTAAAGGGGCTGGA 1343
 DB |||||
 DB 1271 GAGCTGTGCATGAGCAACAGGTAGAGTCCCAAGATCAGAGCGGCTTTTAAAGGGGCTGGA 1330
 DB |||||
 DB 1344 TTTGTACGCTGAGGCTCAACATGAGCTTGTGTGTGCGGCTTGGCCAGAAAGCTGTGA 1403
 DB |||||
 DB 1331 TTTGTACGCTGAGGCTCAACATGAGCTTGTGTGTGCGGCTTGGCCAGAAAGCTGTGA 1390
 DB |||||
 DB 1404 AGATGTCCAGATCTTGTGTGTGCTCAAGACTGAGTCTTAACTTCAAGATGGGATTT 1463
 DB |||||
 DB 1391 AGATGTCCAGATCTTGTGTGTGCTCAAGACTGAGTCTTAACTTCAAGATGGGATTT 1449
 DB |||||
 DB 1464 CCTTACCAAGATTTTGTGACAGACATATATCCAGTACCCAACTATCTGTCTTCAAAAG 1523
 DB |||||
 DB 1450 CCTTACCAAGATTTTGTGACAGACATATATCCAGTACCCAACTATCTGTCTTCAAAAG 1509
 DB |||||
 DB 1524 CCAAGCATGTCTGATGAGAAACCGCAATGAGAAAGTGTCCCGATGATGTCTGCAAAA 1583
 DB |||||

QY 427 GTCTCTATTTCTTCACCTTAACACTCTCAAGAGATAGAGCTTCAAGTCTCAACC 486
DB 415 GTCTCTATTTCTTCACCTTAACACTCTCAAGAGATAGAGCTTCAAGTCTCA-CC 473
QY 487 ACCACGATGACCTCCCATCTTCAACCTTCAAGTACAGAAAGCCAGACTTCCAG 546
DB 474 ACCACGATGACCTCCCATCTTCAACCTTCAAGTACAGAAAGCCAGACTTCCAG 532
QY 547 CCTGTGCTGAGAGGCTCAGCAACAGTGGAGAGCTCTCAAGTCTCTTGTCCCTG 606
DB 533 CCTGTGCTGAGAGGCTCAGCAACAGTGGAGAGCTCTCAAGTCTCTTGTCCCT- 591
QY 607 GAGAGCCAGAGCAAGCCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 666
DB 592 GAGAGCCAGAGCAAGCCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 650
QY 667 CCACACACAAACACAAACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 726
DB 651 CCACACACAAACACAAACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 709
QY 727 GAAGAGAGGAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 786
DB 710 GAAGAGAGGAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 768
QY 787 CAGCTGACAGACAGACTCAGAGCCCAAGTTCCTCTGATCTCTTCTTAACTTCC 846
DB 769 CAGCTGACAGACAGACTCAGAGCCCAAGTTCCTCTGATCTCTTCTTAACTTCC- 827
QY 847 TCTTTTGTCTCCCGGGTACAGAAAGTGAAGTCTTCTCTTATGATATGAGAAATCCAG 906
DB 828 TCTTTTGTCTCCCGGGTACAGAAAGTGAAGTCTTCTCTTATGATATGAGAAATCCAG 886
QY 907 GAGCTCATTTGATCAGGCCAGAAATGATGAATGAATGAATGAATGAATGAATGAATCC 966
DB 887 GAGCTCATTTGATCAGGCCAGAAATGATGAATGAATGAATGAATGAATGAATGAATCC 945
QY 967 TACTGAGAAACCAAAACCTTGCAGCTTCTGACAGTGCCTCCCAACAGAGGCTTGTG 1026
DB 946 TACTGAGAAACCAAAACCTTGCAGCTTCTGACAGTGCCTCCCAACAGAGGCTTGTG- 1003
QY 1027 GTGCTGTCTATTTGATCTGAGAAATGATGAATGAATGAATGAATGAATGAATGAAT 1086
DB 1004 GTGCTGTCTATTTGATCTGAGAAATGATGAATGAATGAATGAATGAATGAATGAAT 1061
QY 1087 AAGTATAGAGAGAGAGATCTTGTGTTGGAGAGTCCGTCTGTGCAACCTTGGGCGG 1146
DB 1062 AAGTATAGAGAGAGAGATCTTGTGTTGGAGAGTCCGTCTGTGCAACCTTGGGCGG- 1119
QY 1147 CGACATATGCTACTGCTGCTCTGCTCTGCTCTTGAAGCTGAGAGAGTGCAGC 1206
DB 1120 CGACATATGCTACTGCTGCTCTGCTCTGCTCTTGAAGCTGAGAGAGTGCAGC- 1177
QY 1207 TCAGAGGCCAGCTGAGCGGCAAAATGCGAACCTTCCCAAGAGCTCTTGTGAGC 1266
DB 1178 TCAGAGGCCAGCTGAGCGGCAAAATGCGAACCTTCCCAAGAGCTCTTGTGAGC- 1235
QY 1267 CCTTGTGCTGCTCCCAAGAGCTGCTCATGCGGCAACAGTGAAGTCCCAAGATCGGC 1326
DB 1236 CCTTGTGCTGCTCCCAAGAGCTGCTCATGCGGCAACAGTGAAGTCCCAAGATCGAG- 1293
QY 1327 CGCTTTTACCGGCTGAGATTTGTACGAGGAGCTCCACATGAGACTTGTGTGCGGCTT 1386
DB 1294 CGCTTTTACCGGCTGAGATTTGTACGAGGAGCTCCACATGAGACTTGTGTGCGGCTT- 1351
QY 1387 GCCACGAAAGGCTGTGAAGATGTCGAGTCTGAGGAGCTGAGAGTGTCTTGAAGC 1446
DB 1352 GCCACGAAAGGCTGTGAAGATGTCGAGTCTGAGGAGCTGAGAGTGTCTTGAAGC- 1409
QY 1447 TTCAGAGAGGAGATTTCCCTACCAAGATTTGTGAACAACAATATCCAGTATCCCAAC 1506
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QY 1507 TACTGTCTCTTCAAAAGCCAGAGTGTCTGATGAGAAACCGCAATCGGAAGTGTCCGC 1566

DB 1468 TACTGTCTCTTCAAAAGCCAGAGTGTCTGATGAGAAACCGCAATCGGAAGTGTCC- 1525
QY 1567 ATGAGATGCTGCAAGATGAGACTTACAGTCCGCTGAGCCCTGCAAAAGTGAAGAGT 1626
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DB 1585 G-CTTGTGATGAGAGCCAGAGTTCAGACCTTGAAGTGAAGCCAGTTCGAGTGAAGTGC- 1641
QY 1687 GTCTATTTGCTCCCAACCCCAAGCCCAAGCTTCCCAAGCTTCTATTTGTTGAGACCCA 1746
DB 1642 GTTATTTTGTCCCAACCCCAAGCCCAAGCTTCCCAAGCTTCTATTTGTTGAGACCCA- 1699
QY 1747 TTGCTTCAAGGCTCCCTCTGAGTCTGTTTCTTACCTGCGCCCTACTACATTTCTTGGGT 1806
DB 1700 TTGCTTCAAGGCTCCCTCTGAGTCTGTTTCTTACCTGCGCCCTTATTCATTTCTTGG- 1757
QY 1807 TGAGCAACAGTCCCAAGAGAGGCAAGGAGAGTGGAGCTGCGCCCTCTTAAAGATGACTT 1866
DB 1758 TGAGCAACAGTCCCAAGAGAGGCAAGGAGAGTGGAGAGTGGAGCTGCGCCCTCTTAAAGATGAGC- 1815
QY 1867 TACATAAATGTTGATCTTCAAAAAAAA 1895
DB 1816 TACATAAATGTTGATCTTCAAAAAAAA 1844

RESULT 11

AAH9858 ID AAH9858 standard; cDNA, 1671 BP.

XX AAH9858;

DT 16-OCT-2001 (first entry)

XX Human protein encoding cDNA sequence SEQ ID NO:693.

XX Human, cancer; ulcer; HIV infection; human immunodeficiency virus;
XX anti-inflammatory; antirheumatic; antiarthritic; immunosuppressive;
XX antibacterial; endocrine; cardiac; central nervous system; virucide;
XX anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
XX antiaggregant; haemostatic; vulnery; antitumor; osteopathic; eczema;
XX dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
XX neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
XX immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
XX antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
XX cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
XX thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
XX allergic rhinitis; diabetes; multiple sclerosis; depression;
XX Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
XX neurological disorder; ss.

XX Homo sapiens.

XX NO200153455-A2.

XX 26-JUL-2001.

XX 22-DEC-2000; 2000MO-US035017.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-00552317.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Dymnac RT;

XX WPI, 2001-457603/49.

XX P-PSDB; AAM25917.

XX

CC AAH939166 to AAH939904 encode the human proteins given in AAM52525 to
CC AAH25963. The proteins can have activities based on the tissues and cells
CC they are expressed in, such as: antiinflammatory; antirheumatic;
CC antiarthritic; immunosuppressive; antibacterial;
CC central nervous system; viricide; anti-HIV; fungicide; endocrine; cadiant;
CC cardiovascular; anlaemic; antiagregant; haemostatic; vulnertary;
CC antidiabetic; osteoporectic; dermatological; antiallergic; antistematic;
CC antiparkinsonian; cytosolic; neuroprotective; antidepressant; nootropic;
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders

Sequence 1671 BP; 361 A; 537 C; 424 G; 349 T; 0 U; 0 Other;

Query Match	Score	DB 4	Length
Best Local Similarity	67.1%	1271.8	1671
Matches 1273; Conservative	99.8%	0	3

QY	91	GTGTGCTCCGCGCTCTCGGCACTCGGCCGACGCCGACGATTCGATCTCAAGGCCCCCACTTCA	150
Db	397	GTGTGCTCTCTGCTCTCTGGCACTCTGCGCAGGCCGACGATTCGATCTCAAGGCCCCCACTTCA <td>456</td>	456
QY	151	GGCAGCCCTTCTCTCTCTTACCGAATACGAACGCTTCTTGACATGTGATCTTCAACTGG	210
Db	457	GGAAGCCCTCTCTCTCTACCGAATACGAACGCTTCTTGACATGTGATCTTCAACTGG	516
QY	211	AAGCGAGACTACCTGCGCTCTCCGTCACACCGCGCTCCCGAAATCCCACTGTG	270
Db	517	AAGCGAGACTACCTGCGCTCTCCGTCACACCGCGCTCCCGAAATCCCACTGTG	576
QY	271	CAGCTGACCAATATGAAACAACCGGCTTAGTGCCGATGGTGTGTCTCAACTTC	330
Db	577	CAGCTGACCAATATGAAACAACCGGCTTAGTGCCGATGGTGTGTCTCAACTTC	636
QY	331	CCTTATGCTCTCGTGTGAGCTTCTTCTGCGCAATTCACCTACCTACCGTGTGCAACGAC	390
Db	637	CCTTATGCTCTCGTGTGAGCTTCTTCTGCGCAATTCACCTACCGTGTGCAACGAC	696
QY	391	GTCTACTATGCGCAAGAAGTCTGTGTGTTCCAGCAGTCTCTATTCCTCAACTCACT	450
Db	697	GTCTACTATGCGCAAGAAGTCTGTGTGTTCCAGCAGTCTCTATTCCTCAACTCACT	756
QY	451	CTCAAGAGATAGAAGCTTCAGCTGAAGTCTACCCACCAAGATGACCTCCCACTTCA	510
Db	757	CTCAAGAGATAGAAGCTTCAGCTGAAGTCTACCCACCAAGATGACCTCCCACTTCA	816
QY	511	CCCCACTTCACTGACAGAACGCCAGACCTTTCAGCCTGTGCTGAGAGGTCAGGAC	570
Db	817	CCCCACTTCACTGACAGAACGCCAGACCTTTCAGCCTGTGCTGAGAGGTCAGGAC	876
QY	571	AACGTGAAAGCTCTCACAATCTCTGTCCCTTGGAGGTCAGAGCAAGCCGACAG	630
Db	877	AACGTGAAAGCTCTCTCACAATCTCTGTCCCTTGGAGGTCAGAGCAAGCCGACAG	936
QY	631	CAACAAGAGAGCAAGAGTGTGAGCAAGGCAAGGCCGACACAAAGAAACAAGCAGAA	690
Db	937	CAACAAGAGAGCAAGAGTGTGAGCAAGGCAAGGCCGACACAAAGAAACAAGCAGAA	996

QY	691	GAGGGGCGAAGAACGGAAGACGAAGAGGAACAGGAAGAGAGGAGAAAGCGAGGAAGA	750
Db	997	GAGGGGCGAAGAACGGAAGAGCAAGAGAGGAACAGGAAGAGAGGAAGAGCGAGGAAGA	1056
QY	751	GGACAGAGGACCTAAGAGAGGAGCGGAGGCGTGTCGAGCTGCACACAGACTCAGAGGCC	810
Db	1057	GGACAGAGGAGCTAAGAGAGGAGCGGAGGCGTGTCGTCGAGCTGCACACAGACTCAGAGGCC	1116
QY	811	AAGTTTCACTGTAATCTCTATCTTTAAACCTTTCCTTTTGTGCTCCCGGGTACGAAA	870
Db	1117	AAGTTTCACTGTAATCTCTATCTTTTAAACCTTTCCTTTTGTGCTCCCGGGTACGAAA	1176
QY	871	GTAAGCTTACTCTATGTATATGTAGAAACATCCAGAGCTCATTCGATCAGGCCAGAAA	930
Db	1177	GTAAGCTTACTCTCTATGTATATGTAGAAACATCCAGAGCTCATTCGATCAGGCCAGAAA	1236
QY	931	ATAGATGAATGAATGAATGAATATATATGTAGAACTCTACTGAGAAAACAAAACCTTGCC	990
Db	1237	ATAGATGAATGAATGAATGAATATATATGTAGAACTCTACTGAGAAAACAAAACCTTGCC	1296
QY	991	AGCTTCTGACACCTGCCCCACACAGAGGCTTCTGTGTGTGTCGTAATTCGATCGTGGAG	1050
Db	1297	AGCTTCTGACACCTGCCCCACACAGAGGCTTCTGTGTGTGTCGTAATTCGATCGTGGAG	1356
QY	1051	AATTACCTGCATCAATACCCCCACAGCCACAGGCGCTGGAAGTACATGAGAGAGAGATCCTT	1110
Db	1357	AATTACCTGCATCAATACCCCCACAGGCGCTGGAAGTACATGAGAGAGAGATCCTT	1416
QY	1111	GGTTTCGGGAAGTGGTCTGTGACAGGCTTGGGCGCGACACATGTCTACCTGTGCCCCC	1170
Db	1417	GGTTTCGGGAAGTGGTCTGTGACAGGCTTGGGCGCGACACATGTCTACCTGTGCCCCC	1476
QY	1171	TGTGACTTTCGCTCCTTTGAAGCTGGAAGCAGTGCCTACAGAGGCCAGCGTGAAGGGGAA	1230
Db	1477	TGTGACTTTCGCTCCTTTGAAGCTGGAAGCAGTGCCTACAGAGGCCAGCGTGAAGGGGAA	1536
QY	1231	CAATGGACACCTTCCACAAAGACTCCCTTGTCAAGCCCTTGCCTTGCTCCCAAGGCTG	1290
Db	1537	CAATGGACACCTTCCCAAAAGACTCCCTTGTCAAGCCCTTGCCTTGCTCCCAAGGCTG	1596
QY	1291	TCCATCGGCAACAGGCTAGGGGTCCCAAGATCAGAGCCGCTTTTACGGGCTGGATTTGTAC	1350
Db	1597	TCCATCGGCAACAGGCTAGGGGTCCCAAGATCAGAGCCGCTTTTACGGGCTGGATTTGTAC	1656
QY	1351	GGTGGGCTCCACATG 1365	
Db	1657	GGTGGGCTCCACATG 1671	

RESULT 12
ADO24565
ID ADO24565 standard; cDNA; 3306 BP.
XX

DT 12-AUG-2004 (first entry)
XX

DE	Human	PRO7347	encoding	CDNA	SEQ	ID	NO:204
XX							

KM human; PRO; antianaemic; antiarthritic; antiinflammatory; antipsoriatic;
 KM antirheumatic; dermatological; immunostimulant; immunosuppressive;
 KM osteophytic; vasotropic; immune related disease;
 KM inflammatory immune response; rheumatoid arthritis; osteoarthritis;
 KM juvenile chronic arthritis; systemic lupus erythematosus;
 KM spondyloarthropathy; systemic sclerosis;
 KM idiopathic inflammatory myopathy; Sjögren's syndrome;
 KM systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
 KM autoimmune disease; immune-mediated skin disease; bullous skin disease;
 KM erythema multiforme; contact dermatitis; psoriasis; lymphadenopathy;
 KM splenomegaly; leukopenia; gene; ss.
 OS
 27 Homo sapiens.

AA97739;
 13-SEP-1999 (first entry)
 Extended human secreted protein coding sequence, SEQ ID NO. 304.
 Secreted protein; human; cytokine; cellular proliferation; cell movement;
 cellular differentiation; immune system regulator; anti-inflammatory;
 haematopoiesis regulator; tissue growth regulator; tumour inhibitor;
 reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
 genetic disease; SS.
 Homo sapiens.
 MO9931236-AZ.
 24-JUN-1999.
 17-DEC-1998; 98WO-1B002122.
 17-DEC-1997; 97US-0069957P.
 09-FEB-1998; 98US-0074121P.
 13-APR-1998; 98US-0081563P.
 10-AUG-1998; 98US-0096116P.
 (GEST) GENSET.
 Bougueleret L, Duclert A, Dumas Milne Edwards J;
 WPI; 1999-385906/32.
 P-PSDB; AAY36055.
 New isolated human secreted proteins.
 Claim 1; Page 377; 516pp; English.
 This sequence represents an extended human secreted protein coding
 sequence of the invention. The secreted proteins can be used in treating
 or controlling a variety of human conditions. The secreted proteins may
 act as cytokines or may affect cellular proliferation or differentiation
 or may act as immune system regulators, haematopoiesis regulators, tissue
 growth regulators, regulators of reproductive hormones or cell movement
 or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or
 tumour inhibition activity. The DNAs can be used in forensic procedures
 to identify individuals or in diagnostic procedures to identify
 individuals having genetic diseases resulting from abnormal expression of
 the genes corresponding to the extended cDNAs. They are also useful for
 constructing a high resolution map of the human chromosomes. They can
 also be used for gene therapy to control or treat genetic diseases
 Sequence 964 BP; 258 A; 294 C; 227 G; 180 T; 0 U; 5 Other;
 Query Match 49.4%; Score 937; DB 2; Length 964;
 Best Local Similarity 99.3%; Pred. No. 1.4e-236;
 Matches 948; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
 30 GGGCGATCTTCCGGCCATGAGGAGCGCGCTTCTTCCCTCATCTCTGAA 89
 2 GGGCGATCTTCCGGCCATGAGGAGCGCGCTTCTTCCCTCATCTCTGAA 61
 90 GGTGCTCTCTCTCTGACCTGCGGAGCCAGAGATTGCACTGAGCCCTCC 149
 62 GGTGCTCTCTCTCTGACCTGCGGAGCCAGAGATTGCACTGAGCCCTCC 121
 150 AGGAGGCTCTCTCTCTGACCTGCGGAGCCAGAGATTGCACTGAGCCCT 209
 122 AGGAGGCTCTCTCTCTGACCTGCGGAGCCAGAGATTGCACTGAGCCCT 181
 210 GAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 269
 182 GAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 241
 270 CGAGCTGAGCAATATGAAAAACACGCGTTAGTGCCGATGTGTCTTCAACT 329

|||||
 242 CCAGCTGACCAATATGAAAAACACGCGTTAGTGCCGATGTGTCTTCAACT 301
 330 CCCTTATGCTCTCTGTTGAGTCTTTGCGAGTTCACTCAGTCGTTGTCACCA 389
 302 CCTTATGCTCTCTGTTGAGTCTTTGCGAGTTCACTCAGTCGTTGTCACCA 361
 390 CGTCTATGCGCAAGAGAGTCTGTGTTCCAGCAGTCTATTTCTCACTTAAC 449
 362 GGTCTATGCGCAAGAGAGTCTGTGTTCCAGCAGTCTATTTCTCACTTAAC 421
 450 TCTCAAGAGATGAAAGCTTCACTGAGTCTCACTCACTCACTCACTCACT 508
 422 TCTCAAGAGATGAAAGCTTCACTGAGTCTCACTCACTCACTCACTCACT 481
 509 CACCCCACTTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 568
 482 CACCCCACTTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 541
 569 ACAAGTGAAGAGTCTCTTCAATCTCTCTCTCTCTCTCTCTCTCTCTCT 628
 542 ACAAGTGAAGAGTCTCTTCAATCTCTCTCTCTCTCTCTCTCTCTCTCT 601
 629 AGCAACAAG 688
 602 AGCAACAAG 661
 689 AAG 748
 662 AAG 721
 749 AAG 808
 722 AAG 781
 809 CCAAGTTTCACTGATCTTATCTTCTTAACTCTTCTTCTTCTTCTTCT 868
 782 CCAAGTTTCACTGATCTTATCTTCTTAACTCTTCTTCTTCTTCTTCT 841
 869 AAGTAAAGTCTTCTTATGATATGAGAGAGAGAGAGAGAGAGAGAGAG 928
 842 AAGTAAAGTCTTCTTATGATATGAGAGAGAGAGAGAGAGAGAGAGAG 901
 929 AAGTAAAGTCTTCTTATGATATGAGAGAGAGAGAGAGAGAGAGAGAG 983
 902 AAGTAAAGTCTTCTTATGATATGAGAGAGAGAGAGAGAGAGAGAGAG 956
 RESULT 15
 AD053839
 ID AD053839 standard; DNA; 695 BP.
 AC AD053839;
 XX 21-OCT-2004 (first entry)
 DE Novel canine microarray-related DNA sequence SeqID5141.
 XX canine microarray; drug screening; toxicity assay;
 XX environmental pollutant; cellular response; gene expression profile;
 XX toxic response; liver necrosis; fatty liver disease;
 XX protein adduct formation; hepatitis; dog; ds.
 OS Canis familiaris.
 PN WO2004063324-A2.
 XX 29-JUL-2004.
 XX 05-MAY-2003; 2003WO-US013853.
 XX 03-MAY-2002; 2002US-0377240P.
 XX

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2005, 17:40:21 ; Search time 1053 Seconds
(without alignments)
10653.286 Million cell updates/sec

Title: US-09-559-013E-23

Sequence: 1895
1 gttagagcgctgtgtcc.....tgtagcttcaaaaaaa 1895

Scoring table: OLIGO_NTC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

N_Geneseq_16Dec04:*
1: geneseqn1808:*
2: geneseqn1390s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1895	100.0	1895	5	AAD08658 Human can
2	1886	99.5	1886	6	ABT14679 Human can
3	1742	91.9	1912	3	AAZ50927 Human Pro
4	1494	78.8	1889	2	AAZ06785 Human adu
5	1284	67.8	1882	2	AAZ24890 Human sec
6	1284	67.8	1892	8	ADA39940 Human sec
7	1284	67.8	1892	10	ADC73578 Human sec
8	1284	67.8	1892	10	ADC73578 Human sec
9	1284	67.8	1892	10	ADA56130 Gene enco
10	1173	61.9	1671	4	AAH99858 Human pro
11	536	28.3	3306	12	AD024565 Human PRO
12	528	27.9	964	2	AAH97739 Extended
13	528	27.9	964	12	ADP19006 Human sec
14	379	20.0	469	9	ACH27630 Human adu
15	339	17.9	474	8	ABZ72003 Human ful
16	307	16.2	474	9	ACH49259 Human leu
17	281	14.8	308	2	AAV68163 EST clone
18	280	14.8	507	8	ABZ71923 Human can
19	280	14.8	522	8	ABZ71705 Human can
20	199	10.5	199	8	ABZ19225 Group III

21	116	6.1	1854	9	ADA45034	ADA45034 Human pol
22	112	5.9	128	2	AAZ51481	AAZ51481 Human sec
23	63	3.3	387	8	ABZ19899	ABZ19899 Group III
24	60	3.2	60	6	ABNA9513	ABNA9513 Human spl
25	31	1.6	695	13	AD053839	AD053839 Novel can
26	27	1.4	29	2	AAZ06795	AAZ06795 Human sec
27	27	1.4	29	9	ADA45049	ADA45049 Human o11
28	23	1.2	23	5	AAD08668	AAD08668 Human OY-
29	23	1.2	345	6	ABZ51553	ABZ51553 Human CDN
30	22	1.2	22	5	AAD08665	AAD08665 Human tes
31	21	1.1	21	5	AAD08664	AAD08664 Human tes
32	21	1.1	450	10	ADP80420	ADP80420 Leukaemia
33	21	1.1	249	3	AAZ76271	AAZ76271 Human ORF
34	21	1.1	2684	13	ACNA40762	ACNA40762 Tumour-as
35	21	1.1	28564	10	ADZ63335	ADZ63335 Human gen
36	21	1.1	59767	13	AAZ32905	AAZ32905 Mouse can
37	20	1.1	20	5	AAD08663	AAD08663 Human OY-
38	20	1.1	20	5	AAD08662	AAD08662 ht-3 RT-P
39	20	1.1	20	5	AAD08661	AAD08661 ht-5 RT-P
40	20	1.1	20	5	AAD08666	AAD08666 Human tes
41	20	1.1	20	8	ABT14665	ABT14665 Human can
42	20	1.1	20	8	ABT14665	ABT14665 Human can
43	20	1.1	466	4	AAZ33554	AAZ33554 Human bon
44	20	1.1	466	4	ABZ33337	ABZ33337 Human liv
45	20	1.1	466	6	ABZ08423	ABZ08423 Human ant
46	20	1.1	738	12	ADQ27055	ADQ27055 Human ant
47	20	1.1	792	11	ABD01111	ABD01111 Klebsiell
48	20	1.1	1364	6	ABN98242	ABN98242 Arabidops
49	20	1.1	1701	11	ABD01223	ABD01223 Klebsiell
50	20	1.1	3094	4	ABZ74444	ABZ74444 Drosophil
51	20	1.1	3471	10	ADA53602	ADA53602 Human cod
52	20	1.1	5235	12	ADM31027	ADM31027 Human cal
53	20	1.1	6232	2	AAQ29269	AAQ29269 Human cal
54	20	1.1	6792	12	ADM31025	ADM31025 Human cal
55	20	1.1	7175	2	AAQ37818	AAQ37818 Sequence
56	20	1.1	7175	2	AAQ84658	AAQ84658 Human neu
57	20	1.1	7175	2	AAV42686	AAV42686 DNA encod
58	20	1.1	7175	3	AAZ71704	AAZ71704 Human cal
59	20	1.1	7175	6	AAZ39956	AAZ39956 Human cal
60	20	1.1	7175	12	ADJ38318	ADJ38318 Human cal
61	20	1.1	7175	12	ADM57706	ADM57706 Human cal
62	20	1.1	7177	8	ABZ58367	ABZ58367 Human N-t
63	20	1.1	7266	2	AAV29059	AAV29059 Human cal
64	20	1.1	7362	2	AAQ37817	AAQ37817 Sequence
65	20	1.1	7362	2	AAQ84657	AAQ84657 Human neu
66	20	1.1	7362	2	AAZ42685	AAZ42685 DNA encod
67	20	1.1	7362	3	AAZ71703	AAZ71703 Human cal
68	20	1.1	7362	6	AAZ39955	AAZ39955 Human cal
69	20	1.1	7362	12	ADJ38316	ADJ38316 Human cal
70	20	1.1	7362	12	ADM57705	ADM57705 Human cal
71	20	1.1	7363	12	ADQ22372	ADQ22372 Human sof
72	20	1.1	7364	6	ABZ5869	ABZ5869 Lung canc
73	20	1.1	7364	8	ABZ58366	ABZ58366 Human N-t
74	20	1.1	7364	12	ADP21335	ADP21335 Gene CACN
75	20	1.1	7364	13	ADZ43909	ADZ43909 Human N-t
76	20	1.1	7376	2	AAZ88001	AAZ88001 N-type ca
77	20	1.1	7376	13	ADR43931	ADR43931 N-type ca
78	20	1.1	26214	12	ADQ97246	ADQ97246 Mouse can
79	20	1.1	72352	12	ADQ97067	ADQ97067 Mouse can
80	20	1.1	72352	11	ACNA4076	ACNA4076 Mouse gen
81	20	1.1	110000	11	ACNA42475	ACNA42475 (3 of
82	20	1.1	198073	11	ACNA43302	ACNA43302 Human gen
83	19	1.0	19	5	AAD08667	AAD08667 Human OY-
84	19	1.0	252	10	ACF69362	ACF69362 Phototrab
85	19	1.0	307	12	ADH00168	ADH00168 Bovine ES
86	19	1.0	334	8	ABZ37455	ABZ37455 Bovine ES
87	19	1.0	367	3	AAZ27942	AAZ27942 Human sec
88	19	1.0	378	6	ABZ22892	ABZ22892 Human ORF
89	19	1.0	440	8	ABZ65257	ABZ65257 Human gen
90	19	1.0	603	3	AAZ80160	AAZ80160 Human col
91	19	1.0	711	12	ADQ35812	ADQ35812 Novel mou
92	19	1.0	963	5	AAZ63215	AAZ63215 Human pur
93	19	1.0	1069	5	AAZ87758	AAZ87758 DNA encod

94	19	1.0	1069	5	AA878277	AA878277 DNA encod	C 167	18	0.9	100	8	ACD72083	Actd2083 E. coli K
95	19	1.0	1112	3	AA876384	AA876384 Human ORF	C 168	18	0.9	100	8	ACD78582	Actd7852 E. coli K
96	19	1.0	1287	3	AA89404	AA89404 Beta-prim	C 169	18	0.9	100	8	ACD78583	Actd7853 E. coli K
97	19	1.0	1521	3	AA89407	AA89407 Open read	C 170	18	0.9	155	3	ADF57263	Adf57263 Urogenita
98	19	1.0	1595	13	ACN38532	ACN38532 Tumour-as	C 171	18	0.9	157	3	ACAC13527	Acac13527 Human sec
99	19	1.0	1665	8	ACCA4709	ACCA4709 Prokaryot	C 172	18	0.9	175	5	ABAI2653	Abai2653 Human nec
100	19	1.0	1713	10	ADFO0423	ADFO0423 Bacterial	C 173	18	0.9	191	3	ACAC16726	Acac16726 Human nec
101	19	1.0	1834	5	ACA39756	ACA39756 Prokaryot	C 174	18	0.9	201	13	ADBS38781	Adbs38781 Human sec
102	19	1.0	1834	5	AA868454	AA868454 DNA encod	C 175	18	0.9	227	6	ABK39586	Abk39586 Human aut
103	19	1.0	2000	6	ABZ15642	ABZ15642 Arabidops	C 176	18	0.9	227	8	ACAI1932	Acac1932 Human lun
104	19	1.0	2139	8	ACA20568	ACA20568 Prokaryot	C 177	18	0.9	227	8	ACAI1935	Acac1935 Human lun
105	19	1.0	2201	13	ACN39007	ACN39007 Tumour-as	C 178	18	0.9	227	8	ACAI03118	Acac03118 Lung can
106	19	1.0	2201	13	ACN39383	ACN39383 Tumour-as	C 179	18	0.9	227	8	ACAI03101	Acac03101 Lung can
107	19	1.0	2236	4	ABE09505	ABE09505 Drosophi	C 180	18	0.9	227	10	ADH47143	Adh47143 Human lun
108	19	1.0	2570	4	ABE09393	ABE09393 Drosophi	C 181	18	0.9	227	10	ADH47160	Adh47160 Human lun
109	19	1.0	2597	4	AA866902	AA866902 Human EXM	C 182	18	0.9	227	13	ADJ21079	Adj21079 Human lun
110	19	1.0	2652	5	AA885132	AA885132 DNA encod	C 183	18	0.9	227	13	ADJ21062	Adj21062 Human lun
111	19	1.0	2652	10	ADBE0933	ADBE0933 Novel DNA	C 184	18	0.9	227	13	AA126833	AA126833 Probe #16
112	19	1.0	2665	4	AAH16002	AAH16002 Rns p21 i	C 185	18	0.9	244	4	ABK75085	Abk75085 Human foe
113	19	1.0	2671	2	AAZ09608	AAZ09608 Human RGL	C 186	18	0.9	244	4	AAI55620	AAI55620 Probe #24
114	19	1.0	2671	2	AAZ09608	AAZ09608 Human RGL	C 187	18	0.9	244	4	ABK39769	Abk39769 Human bon
115	19	1.0	3076	4	AAH18516	AAH18516 Human PDI	C 188	18	0.9	244	4	AAK439727	AAK439727 Human bon
116	19	1.0	3080	4	AA891322	AA891322 Human PDI	C 189	18	0.9	244	4	ABK3600	Abk3600 Human bra
117	19	1.0	3975	4	AAK94374	AAK94374 Human Full	C 190	18	0.9	244	4	ABK3600	Abk3600 Human bra
118	19	1.0	3975	12	ADL31072	ADL31072 Full leng	C 191	18	0.9	244	4	ABK3600	Abk3600 Human bra
119	19	1.0	4028	5	ADM19259	ADM19259 Novel hum	C 192	18	0.9	244	4	ABK3600	Abk3600 Human bra
120	19	1.0	4068	6	ABN59810	ABN59810 Novel hum	C 193	18	0.9	244	4	ABK3600	Abk3600 Human bra
121	19	1.0	4088	5	ADL62737	ADL62737 Human ova	C 194	18	0.9	329	3	ABN18876	Abn18876 Human ORF
122	19	1.0	4383	4	ABE09783	ABE09783 Drosophi	C 195	18	0.9	329	3	AA856980	AA856980 Plms rad
123	19	1.0	4408	10	ADG28471	ADG28471 Rubella v	C 196	18	0.9	348	3	AA857020	AA857020 Plms rad
124	19	1.0	5076	5	AA868170	AA868170 DNA encod	C 197	18	0.9	388	10	ACD95643	ACD95643 Human sec
125	19	1.0	5076	5	AA882123	AA882123 DNA encod	C 198	18	0.9	448	5	AA876690	AA876690 DNA encod
126	19	1.0	5076	5	AA872828	AA872828 DNA encod	C 199	18	0.9	454	5	AA879988	AA879988 DNA encod
127	19	1.0	5076	5	AA870245	AA870245 DNA encod	C 200	18	0.9	454	5	AA879988	AA879988 DNA encod
128	19	1.0	5076	5	AA874989	AA874989 DNA encod	C 201	18	0.9	461	11	ADT94743	ADT94743 Human col
129	19	1.0	5178	5	AA878732	AA878732 DNA encod	C 202	18	0.9	463	9	ACH45506	ACH45506 Human foe
130	19	1.0	6056	6	ABK33027	ABK33027 Human imm	C 203	18	0.9	471	13	AD895013	AD895013 Human the
131	19	1.0	6160	12	ADJ12530	ADJ12530 DNA fragm	C 204	18	0.9	472	8	ABZ36648	ABZ36648 Human GEN
132	19	1.0	6279	4	ABE09392	ABE09392 Drosophi	C 205	18	0.9	474	5	AA876690	AA876690 DNA encod
133	19	1.0	6480	10	ABZ67665	ABZ67665 Human sec	C 206	18	0.9	474	5	AA876690	AA876690 DNA encod
134	19	1.0	9120	4	ABE09782	ABE09782 Drosophi	C 207	18	0.9	474	5	AA876690	AA876690 DNA encod
135	19	1.0	9588	10	ADG37082	ADG37082 Vector pP	C 208	18	0.9	498	5	AA877936	AA877936 DNA encod
136	19	1.0	9661	2	AAO95904	AAO95904 Drosophi	C 209	18	0.9	502	12	ACH73203	ACH73203 Human gen
137	19	1.0	9757	2	AAO97686	AAO97686 Infection	C 210	18	0.9	502	12	ACH73203	ACH73203 Human gen
138	19	1.0	9759	2	AAO98643	AAO98643 Infection	C 211	18	0.9	504	12	ADN98624	ADN98624 Human gen
139	19	1.0	9759	2	AAO98643	AAO98643 Infection	C 212	18	0.9	504	12	ADN98624	ADN98624 Human gen
140	19	1.0	9759	10	ADG28462	ADG28462 Rubella v	C 213	18	0.9	514	12	ACH73601	ACH73601 Human gen
141	19	1.0	9759	10	ADG28462	ADG28462 Rubella v	C 214	18	0.9	514	12	ACH73601	ACH73601 Human gen
142	19	1.0	9762	3	AAZ48249	AAZ48249 Rubella v	C 215	18	0.9	520	10	ADBS6352	ADBS6352 Human GEN
143	19	1.0	10450	5	AA871127	AA871127 DNA encod	C 216	18	0.9	522	5	AA871834	AA871834 DNA encod
144	19	1.0	10992	4	AAK69375	AAK69375 Human imm	C 217	18	0.9	528	10	ABX57531	ABX57531 Human bon
145	19	1.0	10992	10	ADG37080	ADG37080 Mouse pla	C 218	18	0.9	535	5	AA875559	AA875559 DNA encod
146	19	1.0	36241	10	ADB74385	ADB74385 Mycobacte	C 219	18	0.9	547	5	AA878851	AA878851 DNA encod
147	19	1.0	47613	11	ACNA4072	ACNA4072 Mouse gen	C 220	18	0.9	550	6	ABD31375	ABD31375 Human sec
148	19	1.0	59458	13	ADK67037	ADK67037 Murine ca	C 221	18	0.9	588	12	ACH69097	ACH69097 Human sec
149	19	1.0	59458	13	ADK67037	ADK67037 Murine ca	C 222	18	0.9	597	4	AAI17628	AAI17628 Probe #75
150	19	1.0	63588	8	AB857150	AB857150 Human gen	C 223	18	0.9	597	4	ABK62564	ABK62564 Human foe
151	19	1.0	72705	11	ACNA5158	ACNA5158 Human bre	C 224	18	0.9	597	4	ABK62564	ABK62564 Human foe
152	19	1.0	100267	6	ABE11032	ABE11032 Human bre	C 225	18	0.9	597	4	ABK62564	ABK62564 Human foe
153	19	1.0	100779	10	ACF65386	ACF65386 Mouse can	C 226	18	0.9	597	4	ABK62564	ABK62564 Human foe
154	19	1.0	103471	12	ADQ97668	ADQ97668 Mouse can	C 227	18	0.9	597	4	ABK62564	ABK62564 Human foe
155	19	1.0	110000	4	AAK95240	AAK95240 of	C 228	18	0.9	597	4	ABK62564	ABK62564 Human foe
156	19	1.0	110000	6	ABK96733	ABK96733 of	C 229	18	0.9	597	4	ABK62564	ABK62564 Human foe
157	19	1.0	110000	6	ABK96733	ABK96733 of	C 230	18	0.9	597	4	ABK62564	ABK62564 Human foe
158	19	1.0	110000	6	ABK96733	ABK96733 of	C 231	18	0.9	597	4	ABK62564	ABK62564 Human foe
159	19	1.0	110000	6	ABK96733	ABK96733 of	C 232	18	0.9	597	4	ABK62564	ABK62564 Human foe
160	19	1.0	110000	12	ADH77367	ADH77367 of	C 233	18	0.9	621	5	AA879373	AA879373 Human bon
161	19	1.0	110000	12	ADH77367	ADH77367 of	C 234	18	0.9	621	5	AA879373	AA879373 Human bon
162	19	1.0	110000	12	ADH77367	ADH77367 of	C 235	18	0.9	621	5	AA879373	AA879373 Human bon
163	19	1.0	110000	12	ADH77367	ADH77367 of	C 236	18	0.9	621	5	AA879373	AA879373 Human bon
164	19	1.0	110000	12	ADH77367	ADH77367 of	C 237	18	0.9	621	5	AA879373	AA879373 Human bon
165	19	1.0	110000	12	ADH77367	ADH77367 of	C 238	18	0.9	621	5	AA879373	AA879373 Human bon
166	19	1.0	110000	12	ADH77367	ADH77367 of	C 239	18	0.9	621	5	AA879373	AA879373 Human bon

C 240	18	0.9	663	5	ABV27525	Abv27525 Human pro	C 313	18	0.9	1098	10	ADF57967	Adf57967 Human pol
C 241	18	0.9	667	13	ADQ55795	Adq55795 Novel can	C 314	18	0.9	1104	5	AA581509	AA581509 DNA encod
C 242	18	0.9	669	12	ADP29132	Adp29132 Human sec	C 315	18	0.9	1113	11	ABD05544	ABD05544 Pseudom
C 243	18	0.9	679	6	ABT11384	Abt11384 Yeast bel	C 316	18	0.9	1116	5	AA585777	AA585777 DNA encod
C 244	18	0.9	680	6	ABS62810	Abs62810 Selected	C 317	18	0.9	1120	5	AA579628	AA579628 DNA encod
C 245	18	0.9	681	12	AD000365	Ado00365 Novel hum	C 318	18	0.9	1122	5	AA585423	AA585423 DNA encod
C 246	18	0.9	681	12	ADN98796	Adn98796 Novel hum	C 319	18	0.9	1136	6	ABX97158	Abx97158 Human CNV
C 247	18	0.9	693	5	AA579987	AA579987 DNA encod	C 320	18	0.9	1136	12	ADN62032	Adn62032 Human ova
C 248	18	0.9	694	10	ACD93582	Acd93582 Human col	C 321	18	0.9	1155	5	AA572857	AA572857 DNA encod
C 249	18	0.9	732	5	AA567701	AA567701 DNA encod	C 322	18	0.9	1158	5	AA587752	AA587752 DNA encod
C 250	18	0.9	743	5	AA577336	AA577336 DNA encod	C 323	18	0.9	1162	5	AA570325	AA570325 DNA encod
C 251	18	0.9	749	6	ABT11524	Abt11524 Yeast bel	C 324	18	0.9	1167	5	AA566291	AA566291 DNA encod
C 252	18	0.9	750	6	ABS62919	Abs62919 Selected	C 325	18	0.9	1179	5	AA587847	AA587847 DNA encod
C 253	18	0.9	754	5	AA564911	AA564911 Human sec	C 326	18	0.9	1188	5	AA589552	AA589552 DNA encod
C 254	18	0.9	756	5	AA591722	AA591722 DNA encod	C 327	18	0.9	1189	5	AA587858	AA587858 DNA encod
C 255	18	0.9	756	5	AA587828	AA587828 DNA encod	C 328	18	0.9	1194	5	AA568938	AA568938 DNA encod
C 256	18	0.9	756	5	AA566348	AA566348 DNA encod	C 329	18	0.9	1206	5	AA566357	AA566357 DNA encod
C 257	18	0.9	798	12	AD000447	Ado00447 Novel hum	C 330	18	0.9	1206	5	AA570917	AA570917 DNA encod
C 258	18	0.9	798	12	ADN98878	Adn98878 Novel hum	C 331	18	0.9	1206	5	AA578262	AA578262 DNA encod
C 259	18	0.9	809	5	AA574396	AA574396 DNA encod	C 332	18	0.9	1206	5	AA577459	AA577459 DNA encod
C 260	18	0.9	809	5	AA572025	AA572025 DNA encod	C 333	18	0.9	1206	5	AA577459	AA577459 DNA encod
C 261	18	0.9	826	5	AA571059	AA571059 DNA encod	C 334	18	0.9	1206	10	ADG43735	Adg43735 Human N-a
C 262	18	0.9	833	8	AA515961	AA515961 Human ext	C 335	18	0.9	1223	5	AA571242	AA571242 DNA encod
C 263	18	0.9	834	5	AA587839	AA587839 DNA encod	C 336	18	0.9	1223	5	AA571528	AA571528 DNA encod
C 264	18	0.9	848	10	ADG43737	Adg43737 Human N-a	C 337	18	0.9	1224	5	AA566364	AA566364 DNA encod
C 265	18	0.9	849	10	ADG43732	Adg43732 Human N-a	C 338	18	0.9	1230	5	AA587757	AA587757 DNA encod
C 266	18	0.9	858	5	AA566367	AA566367 DNA encod	C 339	18	0.9	1230	5	AA574408	AA574408 DNA encod
C 267	18	0.9	865	5	AA591659	AA591659 DNA encod	C 340	18	0.9	1230	5	AA579617	AA579617 DNA encod
C 268	18	0.9	870	5	AA569934	AA569934 DNA encod	C 341	18	0.9	1231	5	AA586648	AA586648 DNA encod
C 269	18	0.9	891	5	AA581228	AA581228 DNA encod	C 342	18	0.9	1231	6	ABT07104	Abt07104 Human ova
C 270	18	0.9	895	5	AA570927	AA570927 DNA encod	C 343	18	0.9	1238	8	ABX72982	Abx72982 Human ova
C 271	18	0.9	895	5	AA587853	AA587853 DNA encod	C 344	18	0.9	1263	5	AA579833	AA579833 DNA encod
C 272	18	0.9	895	5	AA577942	AA577942 DNA encod	C 345	18	0.9	1263	5	AA579333	AA579333 DNA encod
C 273	18	0.9	900	5	AA588428	AA588428 DNA encod	C 346	18	0.9	1263	12	ADJ40269	Adj40269 Plant cDN
C 274	18	0.9	930	12	ADN98799	Adn98799 Novel hum	C 347	18	0.9	1266	5	AA585569	AA585569 DNA encod
C 275	18	0.9	930	12	AD000368	Ado00368 Novel hum	C 348	18	0.9	1266	5	AA579624	AA579624 DNA encod
C 276	18	0.9	936	3	AA511939	AA511939 Aspergill	C 349	18	0.9	1266	5	AA577084	AA577084 DNA encod
C 277	18	0.9	936	12	ADP29131	Adp29131 Human sec	C 350	18	0.9	1281	5	AA577933	AA577933 DNA encod
C 278	18	0.9	939	5	AA566384	AA566384 DNA encod	C 351	18	0.9	1281	5	AA576684	AA576684 DNA encod
C 279	18	0.9	942	5	AA571060	AA571060 DNA encod	C 352	18	0.9	1287	5	AA571110	AA571110 DNA encod
C 280	18	0.9	948	5	AA56350	AA56350 DNA encod	C 353	18	0.9	1287	5	AA573976	AA573976 DNA encod
C 281	18	0.9	951	3	AA547433	AA547433 Sequence	C 354	18	0.9	1290	5	AA591670	AA591670 DNA encod
C 282	18	0.9	951	12	ADL12382	Adl12382 Human sec	C 355	18	0.9	1296	5	AA570688	AA570688 DNA encod
C 283	18	0.9	960	2	AA562233	AA562233 Human HAP	C 356	18	0.9	1296	5	AA570926	AA570926 DNA encod
C 284	18	0.9	975	5	AA585563	AA585563 DNA encod	C 357	18	0.9	1302	11	ABD05854	ABD05854 Pseudom
C 285	18	0.9	981	10	ADG12659	Adg12659 Human GPC	C 358	18	0.9	1303	5	AA570697	AA570697 DNA encod
C 286	18	0.9	981	10	ADG43734	Adg43734 Human N-a	C 359	18	0.9	1308	10	ACF70488	Act70488 Phototrab
C 287	18	0.9	983	3	AA559716	AA559716 Human sec	C 360	18	0.9	1311	5	AA566372	AA566372 DNA encod
C 288	18	0.9	987	10	ADG43738	Adg43738 Human N-a	C 361	18	0.9	1314	10	AA579606	AA579606 MDDT re1a
C 289	18	0.9	1000	6	ABN96965	Abn96965 Gene #346	C 362	18	0.9	1314	11	ABD05686	ABD05686 Pseudom
C 290	18	0.9	1000	13	ADR83512	Adr83512 Human pol	C 363	18	0.9	1314	13	ADT48908	Adt48908 Bacteri
C 291	18	0.9	1012	6	AB551033	Ab551033 Human cDN	C 364	18	0.9	1323	5	AA577935	AA577935 DNA encod
C 292	18	0.9	1014	8	ACA51828	Aca51828 Prokaryot	C 365	18	0.9	1326	5	AA566286	AA566286 DNA encod
C 293	18	0.9	1017	12	ADN98784	Adn98784 Novel hum	C 366	18	0.9	1341	5	AA588755	AA588755 DNA encod
C 294	18	0.9	1017	12	AD000353	Ado00353 Novel hum	C 367	18	0.9	1341	5	AA569190	AA569190 DNA encod
C 295	18	0.9	1017	12	ADP28802	Adp28802 Human sec	C 368	18	0.9	1341	5	AA577938	AA577938 DNA encod
C 296	18	0.9	1024	10	AB578336	Ab578336 Toxiciolog	C 369	18	0.9	1347	5	AA584788	AA584788 DNA encod
C 297	18	0.9	1027	5	AA577087	AA577087 DNA encod	C 370	18	0.9	1356	5	AA584788	AA584788 DNA encod
C 298	18	0.9	1032	5	AA575883	AA575883 DNA encod	C 371	18	0.9	1356	5	AA587831	AA587831 DNA encod
C 299	18	0.9	1035	5	AA569354	AA569354 DNA encod	C 372	18	0.9	1356	5	AA579835	AA579835 DNA encod
C 300	18	0.9	1035	5	AA588160	AA588160 DNA encod	C 373	18	0.9	1356	5	AA566356	AA566356 DNA encod
C 301	18	0.9	1035	5	AA579632	AA579632 DNA encod	C 374	18	0.9	1356	5	AA579330	AA579330 DNA encod
C 302	18	0.9	1041	5	AA566287	AA566287 DNA encod	C 375	18	0.9	1356	5	AA566285	AA566285 DNA encod
C 303	18	0.9	1050	8	ACA19022	Aca19022 Prokaryot	C 376	18	0.9	1359	5	AA584438	AA584438 DNA encod
C 304	18	0.9	1050	13	AD546033	Ad546033 Bacteri	C 377	18	0.9	1359	10	ADT59865	Adt59865 Human con
C 305	18	0.9	1052	4	ABK42676	Abk42676 Genomic B	C 378	18	0.9	1360	6	AA552255	AA552255 Human TRN
C 306	18	0.9	1052	5	ADB60832	Adb60832 Connectiv	C 379	18	0.9	1374	5	AA566369	AA566369 DNA encod
C 307	18	0.9	1056	5	AA571111	AA571111 DNA encod	C 380	18	0.9	1378	5	AA573459	AA573459 DNA encod
C 308	18	0.9	1056	5	AA566293	AA566293 DNA encod	C 381	18	0.9	1382	5	AA574298	AA574298 DNA encod
C 309	18	0.9	1060	8	ACA48714	Aca48714 Prokaryot	C 382	18	0.9	1387	5	AA583016	AA583016 DNA encod
C 310	18	0.9	1074	5	AA566375	AA566375 DNA encod	C 383	18	0.9	1395	5	AA577085	AA577085 DNA encod
C 311	18	0.9	1080	5	AA571779	AA571779 DNA encod	C 384	18	0.9	1395	5	AA577941	AA577941 DNA encod
C 312	18	0.9	1095	5	AA578001	AA578001 DNA encod	C 385	18	0.9	1395	5	AA575885	AA575885 DNA encod

[illegible]

C 532	18	0.9	1871	8	ABX98805	Abx98805	Novel	hum	C 605	1871	9	ACF24250	ACF24250	Human	sec
C 533	18	0.9	1871	8	ACA67316	ACA67316	CDNA	enco	C 606	1871	9	ACF63561	ACF63561	Human	sec
C 534	18	0.9	1871	8	ACC81282	ACC81282	Human	sec	C 607	1871	9	ACF50435	ACF50435	Human	sec
C 535	18	0.9	1871	8	ACA95606	ACA95606	Novel	hum	C 608	1871	9	ACH07906	ACH07906	Human	sec
C 536	18	0.9	1871	8	ACD04524	ACD04524	Novel	hum	C 609	1871	9	ACF13712	ACF13712	Human	sec
C 537	18	0.9	1871	8	ACC87965	ACC87965	Human	sec	C 610	1871	9	ACD41638	ACD41638	Human	sec
C 538	18	0.9	1871	8	ACF12627	ACF12627	Human	sec	C 611	1871	9	ACF32051	ACF32051	Human	sec
C 539	18	0.9	1871	8	ACH66289	ACH66289	Novel	hum	C 612	1871	9	ACF23329	ACF23329	Human	sec
C 540	18	0.9	1871	8	ACA96342	ACA96342	Novel	hum	C 613	1871	9	ACF40019	ACF40019	Human	sec
C 541	18	0.9	1871	8	ACA65116	ACA65116	Human	PRO	C 614	1871	9	ACD45541	ACD45541	Human	sec
C 542	18	0.9	1871	8	ACA73842	ACA73842	Human	sec	C 615	1871	9	ACF53198	ACF53198	Human	sec
C 543	18	0.9	1871	8	ACA74254	ACA74254	Novel	hum	C 616	1871	9	ACF27378	ACF27378	Human	sec
C 544	18	0.9	1871	8	ACA96649	ACA96649	Human	PRO	C 617	1871	9	ACF45216	ACF45216	Human	sec
C 545	18	0.9	1871	8	ACD10755	ACD10755	CDNA	enco	C 618	1871	9	ACF29834	ACF29834	Human	sec
C 546	18	0.9	1871	8	ACC91451	ACC91451	Human	sec	C 619	1871	9	ACD89910	ACD89910	Human	sec
C 547	18	0.9	1871	8	ACD02786	ACD02786	CDNA	enco	C 620	1871	9	ACD84691	ACD84691	Human	PRO
C 548	18	0.9	1871	8	ACC87351	ACC87351	Human	sec	C 621	1871	9	ACD98851	ACD98851	CDNA	enco
C 549	18	0.9	1871	8	ACC85935	ACC85935	Human	sec	C 622	1871	9	ACF77143	ACF77143	Human	sec
C 550	18	0.9	1871	8	ACA65423	ACA65423	Human	PRO	C 623	1871	9	ACF76836	ACF76836	Human	sec
C 551	18	0.9	1871	8	ACA94240	ACA94240	Human	sec	C 624	1871	9	ACF49821	ACF49821	Human	sec
C 552	18	0.9	1871	8	ACA97984	ACA97984	Human	PRO	C 625	1871	9	ACF50128	ACF50128	Human	sec
C 553	18	0.9	1871	8	ACA91486	ACA91486	Novel	hum	C 626	1871	9	ACD09527	ACD09527	Human	sec
C 554	18	0.9	1871	8	ACA90700	ACA90700	Novel	hum	C 627	1871	9	ACD08606	ACD08606	Human	sec
C 555	18	0.9	1871	8	ACD16247	ACD16247	Human	sec	C 628	1871	9	ACH03621	ACH03621	Human	sec
C 556	18	0.9	1871	8	ACD17408	ACD17408	Human	sec	C 629	1871	9	ACF12320	ACF12320	Human	sec
C 557	18	0.9	1871	8	ACC92065	ACC92065	Human	sec	C 630	1871	9	ACC94828	ACC94828	Human	sec
C 558	18	0.9	1871	8	ACD02343	ACD02343	Novel	hum	C 631	1871	9	ACD22547	ACD22547	Human	sec
C 559	18	0.9	1871	8	ACA74922	ACA74922	CDNA	enco	C 632	1871	9	ACF15247	ACF15247	Human	sec
C 560	18	0.9	1871	8	ACA91793	ACA91793	Human	PRO	C 633	1871	9	ACC97342	ACC97342	Human	sec
C 561	18	0.9	1871	8	ACA89334	ACA89334	Novel	hum	C 634	1871	9	ACC92372	ACC92372	Human	sec
C 562	18	0.9	1871	8	ACA71437	ACA71437	Human	sec	C 635	1871	9	ACF14019	ACF14019	Human	sec
C 563	18	0.9	1871	8	ACC90837	ACC90837	Human	sec	C 636	1871	9	ACF14326	ACF14326	Human	sec
C 564	18	0.9	1871	8	ACA65847	ACA65847	CDNA	enco	C 637	1871	9	ACF09557	ACF09557	Human	sec
C 565	18	0.9	1871	8	ACA68971	ACA68971	Novel	hum	C 638	1871	9	ACD68394	ACD68394	Novel	hum
C 566	18	0.9	1871	8	ACA94992	ACA94992	CDNA	enco	C 639	1871	9	ACD45848	ACD45848	Human	sec
C 567	18	0.9	1871	8	ACD16554	ACD16554	Human	sec	C 640	1871	9	ACD47997	ACD47997	Human	sec
C 568	18	0.9	1871	8	ACD15633	ACD15633	Human	sec	C 641	1871	9	ACD67728	ACD67728	CDNA	enco
C 569	18	0.9	1871	8	ACA98493	ACA98493	Human	PRO	C 642	1871	9	ACF25536	ACF25536	Human	sec
C 570	18	0.9	1871	8	ABX16736	ABX16736	Human	CDN	C 643	1871	9	ACF29220	ACF29220	Human	sec
C 571	18	0.9	1871	8	ACA63418	ACA63418	Human	PRO	C 644	1871	9	ACD84998	ACD84998	Human	sec
C 572	18	0.9	1871	9	ACA97677	ACA97677	Human	PRO	C 645	1871	9	ACD84077	ACD84077	Human	PRO
C 573	18	0.9	1871	9	ACA99126	ACA99126	Novel	hum	C 646	1871	9	ACD88068	ACD88068	Human	sec
C 574	18	0.9	1871	9	ACC91758	ACC91758	Human	sec	C 647	1871	9	ACF30755	ACF30755	Human	sec
C 575	18	0.9	1871	9	ACD11169	ACD11169	Novel	hum	C 648	1871	9	ACF32358	ACF32358	Human	sec
C 576	18	0.9	1871	9	ACD15019	ACD15019	Human	sec	C 649	1871	9	ACH12018	ACH12018	CDNA	enco
C 577	18	0.9	1871	9	ACD11783	ACD11783	Human	sec	C 650	1871	9	ACH12325	ACH12325	CDNA	enco
C 578	18	0.9	1871	9	ACC95912	ACC95912	Human	sec	C 651	1871	9	ADAI9953	ADAI9953	Novel	hum
C 579	18	0.9	1871	9	ACF16475	ACF16475	Human	sec	C 652	1871	9	ACD40717	ACD40717	Human	sec
C 580	18	0.9	1871	9	ACF02593	ACF02593	Human	sec	C 653	1871	9	ADBI7336	ADBI7336	Human	CDN
C 581	18	0.9	1871	9	ACF02900	ACF02900	Human	sec	C 654	1871	9	ACF18189	ACF18189	Human	sec
C 582	18	0.9	1871	9	ACF21487	ACF21487	Human	sec	C 655	1871	9	ACF08636	ACF08636	Human	sec
C 583	18	0.9	1871	9	ACF10171	ACF10171	Human	sec	C 656	1871	9	ACF31437	ACF31437	Human	sec
C 584	18	0.9	1871	9	ACF78064	ACF78064	Human	sec	C 657	1871	9	ACF52277	ACF52277	Human	sec
C 585	18	0.9	1871	9	ACD46769	ACD46769	Human	sec	C 658	1871	9	ACD50146	ACD50146	Human	sec
C 586	18	0.9	1871	9	ACD49532	ACD49532	Human	sec	C 659	1871	9	ACF38849	ACF38849	Human	sec
C 587	18	0.9	1871	9	ACF28239	ACF28239	Human	sec	C 660	1871	9	ACF26764	ACF26764	Human	sec
C 588	18	0.9	1871	9	ACD88989	ACD88989	Human	sec	C 661	1871	9	ACF24864	ACF24864	Human	sec
C 589	18	0.9	1871	9	ACD84384	ACD84384	Human	PRO	C 662	1871	9	ACF46444	ACF46444	Human	sec
C 590	18	0.9	1871	9	ACD99158	ACD99158	CDNA	enco	C 663	1871	9	ACF27992	ACF27992	Human	sec
C 591	18	0.9	1871	9	ADA78053	ADA78053	Human	sec	C 664	1871	9	ACD89296	ACD89296	Human	sec
C 592	18	0.9	1871	9	ACF48900	ACF48900	Human	sec	C 665	1871	9	ACF63868	ACF63868	Human	sec
C 593	18	0.9	1871	9	ACD09220	ACD09220	Human	sec	C 666	1871	9	ACF60508	ACF60508	Human	sec
C 594	18	0.9	1871	9	ACF12013	ACF12013	Human	sec	C 667	1871	9	ACH12632	ACH12632	CDNA	enco
C 595	18	0.9	1871	9	ACF41247	ACF41247	Human	sec	C 668	1871	9	ACH10055	ACH10055	Human	sec
C 596	18	0.9	1871	9	ACF15861	ACF15861	Human	sec	C 669	1871	9	ACD03910	ACD03910	Human	sec
C 597	18	0.9	1871	9	ACF16168	ACF16168	Human	sec	C 670	1871	9	ACD10448	ACD10448	Human	sec
C 598	18	0.9	1871	9	ADBI7148	ADBI7148	Human	CDN	C 671	1871	9	ACD12090	ACD12090	Human	sec
C 599	18	0.9	1871	9	ACD31995	ACD31995	Human	sec	C 672	1871	9	ACF42475	ACF42475	Human	sec
C 600	18	0.9	1871	9	ACF18803	ACF18803	Human	sec	C 673	1871	9	ACF18496	ACF18496	Human	sec
C 601	18	0.9	1871	9	ACF09250	ACF09250	Human	sec	C 674	1871	9	ACF02286	ACF02286	Human	sec
C 602	18	0.9	1871	9	ACF78371	ACF78371	Human	sec	C 675	1871	9	ACF21794	ACF21794	Human	sec
C 603	18	0.9	1871	9	ACF51970	ACF51970	Human	sec	C 676	1871	9	ACF10478	ACF10478	Human	sec
C 604	18	0.9	1871	9	ACF26457	ACF26457	Human	sec	C 677	1871	9	ACF33930	ACF33930	Human	sec

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C 826	18	0.9	1871	9	ACC93600	ACC93600 Human sec	C 899	18	0.9	1871	10	ADCS2419	ADCS2419 Novel hum
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C 846	18	0.9	1871	9	ACF00557	ACF00557 Human sec	C 919	18	0.9	1871	10	ADP95651	ADP95651 Novel hum
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C 848	18	0.9	1871	9	ACFI14633	ACFI14633 Human sec	C 921	18	0.9	1871	10	ADG12466	ADG12466 Novel hum
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C 850	18	0.9	1871	9	ACF78985	ACF78985 Human sec	C 923	18	0.9	1871	10	ADH34149	ADH34149 Novel hum
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C 856	18	0.9	1871	9	ACF37621	ACF37621 Human sec	C 929	18	0.9	1871	10	ADH37489	ADH37489 Novel hum
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C 867	18	0.9	1871	9	ACD22854	ACD22854 Human sec	C 940	18	0.9	1871	10	ADH57426	ADH57426 Novel hum
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C 881	18	0.9	1871	9	ACF60815	ACF60815 Human sec	C 954	18	0.9	1871	10	ADH11138	ADH11138 Human sec
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C 885	18	0.9	1871	9	ACF55961	ACF55961 Human sec	C 958	18	0.9	1871	10	ADH98123	ADH98123 Novel hum
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C 889	18	0.9	1871	10	ACF56575	ACF56575 Human sec	C 962	18	0.9	1871	10	ADH78678	ADH78678 Novel hum
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ALIGNMENTS

RESULT 1
AAD08658
ID AAD08658 standard; cDNA; 1895 BP.
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[illegible]

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QY      781 GTGTCTCAGTGAAGACAGACTAGAGCCAGAGTTTCACTTGAATCTTATCTTCTTAC 840
Db      781 GTGTCTCAGTGAAGACAGACTAGAGCCAGAGTTTCACTTGAATCTTATCTTCTTAC 840
QY      841 CCTTCTCTTTTCTCTCCCGGATACGAGAGTGAAGTCTCTCTATGATATGAGAGAC 900
Db      841 CCTTCTCTTTTCTCTCCCGGATACGAGAGTGAAGTCTCTCTATGATATGAGAGAC 900
QY      901 ATCCAGAGCTCAATTGATCAGCCAGAGAAATGATGAAATGAAATATATATGATGAG 960
Db      901 ATCCAGAGCTCAATTGATCAGCCAGAGAAATGATGAAATGAAATATATATGATGAG 960
QY      961 AACTCTTACTGAGAAACCAAAACCTGAGACTTCTGAGAGCTCCCAACAGAGAGCC 1020
Db      961 AACTCTTACTGAGAAACCAAAACCTGAGACTTCTGAGAGCTCCCAACAGAGAGCC 1020
QY      1021 TTGCTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Db      1021 TTGCTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
QY      1081 GCTTGAAGTACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCTT 1140
Db      1081 GCTTGAAGTACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCTT 1140
QY      1141 GGGCGCGACACATGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Db      1141 GGGCGCGACACATGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
QY      1201 TGGCAGTCAAGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGG 1260
Db      1201 TGGCAGTCAAGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGG 1260
QY      1261 GTGAGCCCTTGTGCTTCCAGAGCTTCCATCGGCAACAGAGTGGGTCCCGAGAA 1320
Db      1261 GTGAGCCCTTGTGCTTCCAGAGCTTCCATCGGCAACAGAGTGGGTCCCGAGAA 1320
QY      1321 TCAGGCGCGCTTTTACCGGCTGATTTGTAAGTGGGCTCCACATGAGCTTCTG 1380
Db      1321 TCAGGCGCGCTTTTACCGGCTGATTTGTAAGTGGGCTCCACATGAGCTTCTG 1380
QY      1381 CGGCTTGGCCAGAAAGGCTGTGAAGATGTCGAGTCTGGGAGGCTCCAGACTGAGTTC 1440
Db      1381 CGGCTTGGCCAGAAAGGCTGTGAAGATGTCGAGTCTGGGAGGCTCCAGACTGAGTTC 1440
QY      1441 CTTAGCTTCCAGAGTGGGATTTCCCTACCAAGATTTGTGACACAGACTATATCCAGTAC 1500
Db      1441 CTTAGCTTCCAGAGTGGGATTTCCCTACCAAGATTTGTGACACAGACTATATCCAGTAC 1500
QY      1501 CCAAACTACTGTTCTTCAAAAGCCAGAGTGTCTGATGAGAAACCGCAATCGAAAGTG 1560
Db      1501 CCAAACTACTGTTCTTCAAAAGCCAGAGTGTCTGATGAGAAACCGCAATCGAAAGTG 1560

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QY      1561 TCCCGCATGAGATGTCTGCAAGATGAGACTTACAGTGCCTGAGCCCTGGCAAAAGTGAG 1620
Db      1561 TCCCGCATGAGATGTCTGCAAGATGAGACTTACAGTGCCTGAGCCCTGGCAAAAGTGAG 1620
QY      1621 GAGGTGTGTGTGATGAGAGCCAGAGATTGAGACCTTGAATCTGAGGCCAGTTGGATGA 1680
Db      1621 GAGGTGTGTGTGATGAGAGCCAGAGATTGAGACCTTGAATCTGAGGCCAGTTGGATGA 1680
QY      1681 GCTGGGCTTATTTCTGGCCACACCCAGCCCACTGCGCCACGTTCTTATTTGTTGAG 1740
Db      1681 GCTGGGCTTATTTCTGGCCACACCCAGCCCACTGCGCCACGTTCTTATTTGTTGAG 1740
QY      1741 ACCCCATTTGCTTTCAGGCTGCCCCCTTGTGGGTCTGTTACTGCGCCCTACTCAATTTCC 1800
Db      1741 ACCCCATTTGCTTTCAGGCTGCCCCCTTGTGGGTCTGTTACTGCGCCCTACTCAATTTCC 1800
QY      1801 TTGGGTTTGAACAACAGTCCCAAGAGAGGCGCAGGTGGAGCTGCGCTCTTAAAGA 1860
Db      1801 TTGGGTTTGAACAACAGTCCCAAGAGAGGCGCAGGTGGAGCTGCGCTCTTAAAGA 1860
QY      1861 TGACTTTACATTAATCTTGAATCTTCAAAAAA 1895
Db      1861 TGACTTTACATTAATCTTGAATCTTCAAAAAA 1895

RESULT 2
ABT14679
ID ABT14679 standard; DNA; 1886 BP.
XX
AC ABT14679;
XX
DT 27-FEB-2003 (first entry)
XX
DE Human cancer-testis antigen coding sequence #6.
XX
KW Human; gene; ds; gene therapy; vaccine; cancer-testis antigen;
CT antigen; breast cancer; colon cancer; cervical cancer; gastric cancer.
XX
OS Homo sapiens.
XX
PN W0200286071-A2.
XX
PD 31-OCT-2002.
XX
PF 19-APR-2002; 2002MO-US012497.
XX
PR 20-APR-2001; 2001US-0285343P.
PR 14-FEB-2002; 2002US-0356937P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Nakayama E, Ono T, Old LJ;
XX
DR WPI; 2003-075624/07.
XX
DR P-PSDB; AAO16118.
XX
PT New cancer-testis (CT) antigens, nucleic acids and encoded polypeptides,
PT useful for diagnosing, monitoring or treating disorder or condition
PT associated with the expression of human CT antigens, e.g. breast cancer
PT or cervical cancer.
XX
PS Example 2; Page 151-154; 165pp; English.
XX
CC The invention comprises the amino acid and coding sequences of human
CC cancer-testis (CT) antigens that bind an HLA molecule. The CT antigens of
CC the invention are useful for diagnosing, monitoring or treating cancer
CC (e.g. breast cancer, colon cancer, cervical cancer or gastric cancer).
CC The present DNA sequence encodes a human cancer-testis (CT) antigen
XX
SQ Sequence 1886 BP; 440 A; 565 C; 481 G; 400 T; 0 U; 0 Other;
Query Match 99.5%; Score 1886; DB 8; Length 1886;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1886; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTTAGAGGAGGCTTGTGCTTCAACGGGACGGGCGGATCTTCTCGGCAATGAGAAAGCA 60
Db 1 GTTAGAGGAGGCTTGTGCTTCAACGGGACGGGCGGATCTTCTCGGCAATGAGAAAGCA 60
QY 61 GCGCGTGGCTTCTTCCCTCACTCTGAAAGTGCTGTCTCTGCTTGGACCTGCGCA 120
Db 61 GCGCGTGGCTTCTTCCCTCACTCTGAAAGTGCTGTCTCTGCTTGGACCTGCGCA 120
QY 121 GCCCAGATTCGACTCAGGCGCCCACTCCAGGAGCCCTCTCTCTACCGAATAGAA 180
Db 121 GCCCAGATTCGACTCAGGCGCCCACTCCAGGAGCCCTCTCTCTACCGAATAGAA 180
QY 181 GCGTCTTGGCACTGCTGACTCCACCTGAAAGGAGAGTACCTGCGCTCTCGTCA 240
Db 181 GCGTCTTGGCACTGCTGACTCCACCTGAAAGGAGAGTACCTGCGCTCTCGTCA 240
QY 241 ACCCAGGCTGCGGGAATCCCACTCTGCTCCAGCTGACCAATATGAAAACAAGCTTA 300
Db 241 ACCCAGGCTGCGGGAATCCCACTCTGCTCCAGCTGACCAATATGAAAACAAGCTTA 300
QY 301 GTGCGGATGCTGCTGCTGCTCCAACTCTCTATGCTCTGCTGCTTGAAGCTTCTG 360
Db 301 GTGCGGATGCTGCTGCTGCTCCAACTCTCTATGCTCTGCTGCTTGAAGCTTCTG 360
QY 361 CAGTTCACTGACTACGTTGCTCCAACTGCTCTACTATGCTCCAGAGAGTCTGTTCC 420
Db 361 CAGTTCACTGACTACGTTGCTCCAACTGCTCTACTATGCTCCAGAGAGTCTGTTCC 420
QY 421 CAGCAGTCTCTATCTCTCACTTCACTTCACTTCAAGAGATGAAAGCTTCAAGCTTA 480
Db 421 CAGCAGTCTCTATCTCTCACTTCACTTCACTTCAAGAGATGAAAGCTTCAAGCTTA 480
QY 481 TCACCCACACAGATGACTCTCCCATCTCACTCCCACTTCAAGTACAGAAACGCGCAG 540
Db 481 TCACCCACACAGATGACTCTCCCATCTCACTCCCACTTCAAGTACAGAAACGCGCAG 540
QY 541 TTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 541 TTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 601 TCCCTGGAGGCGCAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 601 TCCCTGGAGGCGCAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 661 CAGGAGCGGACACAGAAACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 661 CAGGAGCGGACACAGAAACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 GAACAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 721 GAACAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 GTGCTCAGCTGACAGACTCAGAGCCCAAGTTCACTCTGAATCTCTATCTTCTAC 840
Db 781 GTGCTCAGCTGACAGACTCAGAGCCCAAGTTCACTCTGAATCTCTATCTTCTAC 840
QY 841 CTTCTCTTTTGTCTCCCGGGTACGAGAGTGAAGTCTTCTCTCTCTCTCTCTCTAC 900
Db 841 CTTCTCTTTTGTCTCCCGGGTACGAGAGTGAAGTCTTCTCTCTCTCTCTCTCTAC 900
QY 901 ATCCAGAGGCTATTCATCAGCCAGGAAATAGTGAATGAATGAATGAATGAATGA 960
Db 901 ATCCAGAGGCTATTCATCAGCCAGGAAATAGTGAATGAATGAATGAATGAATGA 960
QY 961 AACTCTACTGAGAAACCAAACTCTGAGCTTCTGAGCTGCGCCCAAGAGGCT 1020
Db 961 AACTCTACTGAGAAACCAAACTCTGAGCTTCTGAGCTGCGCCCAAGAGGCT 1020
QY 1021 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 1021 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080

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Db 1021 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
QY 1081 GCTTGAAGTACATGAGAGAGAGATCTGCTGCTTGGGAAAGTGGCTGTGACAGCTT 1140
Db 1081 GCTTGAAGTACATGAGAGAGAGATCTGCTGCTTGGGAAAGTGGCTGTGACAGCTT 1140
QY 1141 GGGCGGACACATGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Db 1141 GGGCGGACACATGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
QY 1201 TGCCATCAGAGGCGCAGCTGCAAGCGGCAACATGCAACCTCCCAAGATCTCTCTT 1260
Db 1201 TGCCATCAGAGGCGCAGCTGCAAGCGGCAACATGCAACCTCCCAAGATCTCTCTT 1260
QY 1261 GTCAGCCCTTGTCTCTCTCCAGAGCTGCTCACTGCGCAACAGTATGAGGTCCCA 1320
Db 1261 GTCAGCCCTTGTCTCTCTCCAGAGCTGCTCACTGCGCAACAGTATGAGGTCCCA 1320
QY 1321 TCAAGGCGCTTTTACGAGCTGAGATTTGATCGGTGGCTCCACATGGACTTGTG 1380
Db 1321 TCAAGGCGCTTTTACGAGCTGAGATTTGATCGGTGGCTCCACATGGACTTGTG 1380
QY 1381 CGGCTTGCCACGAAAGCTGGAAGATGCTCCAGATCTCTGCTGCTGCTGCTGCTG 1440
Db 1381 CGGCTTGCCACGAAAGCTGGAAGATGCTCCAGATCTCTGCTGCTGCTGCTGCTG 1440
QY 1441 CTTAGCTTCCAGAGTGGGAGTTTCTTCAAGATTTGATGACAGACTATATCCAGTAC 1500
Db 1441 CTTAGCTTCCAGAGTGGGAGTTTCTTCAAGATTTGATGACAGACTATATCCAGTAC 1500
QY 1501 CCAAACTATGCTTCTTCAAAAGCCAGAGTGTCTGATGAGAAACCGCAATCGAAGGTG 1560
Db 1501 CCAAACTATGCTTCTTCAAAAGCCAGAGTGTCTGATGAGAAACCGCAATCGAAGGTG 1560
QY 1561 TCCCGATGAGATGCTGCAAGATGAGACTTACAGTGTGCTGAGCTTGTGAGAGAG 1620
Db 1561 TCCCGATGAGATGCTGCAAGATGAGACTTACAGTGTGCTGAGCTTGTGAGAGAG 1620
QY 1621 GAGCTGTCTGCTGATGAGAGCCAGAGTTCAGACCTTGAACCTAGAGCCCTGCA 1680
Db 1621 GAGCTGTCTGCTGATGAGAGCCAGAGTTCAGACCTTGAACCTAGAGCCCTGCA 1680
QY 1681 GCTGGGCTTATTTGCCCAACCCAGCCCAACCTGCTGCTGCTGCTGCTGCTGCTG 1740
Db 1681 GCTGGGCTTATTTGCCCAACCCAGCCCAACCTGCTGCTGCTGCTGCTGCTGCTG 1740
QY 1741 ACCCATGCTTTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
Db 1741 ACCCATGCTTTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
QY 1801 TTGGGTTGAGCAACATCTCCAGAGAGGCGACGAGTGGAGCTGCGCTCTTAAAGA 1860
Db 1801 TTGGGTTGAGCAACATCTCCAGAGAGGCGACGAGTGGAGCTGCGCTCTTAAAGA 1860
QY 1861 TGACTTACATTAATGTTGATCTTC 1886
Db 1861 TGACTTACATTAATGTTGATCTTC 1886

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RESULT 3

AA250927 standard; cDNA; 1912 BP.

AA250927;

05-JUN-2000 (first entry)

Human Protease and associated protein-10 (PRG-10) encoding cDNA.

KW Protease and associated protein-10; PRG-10; anti-PRG antibody;
 KW arteriosclerosis; atherosclerosis; bursitis; hepatitis; immune disorder;
 KW AIDS; Addison's disease; adult respiratory distress syndrome; allergy;

KM ankylosing spondylitis; amyloidosis; cytostatic; antiarteriosclerotic;
 KM hepatocarcinoma; antineoplastic; virucide; antiparasitic; anti-HIV;
 KM antiallergic; immunosuppressive; antidiabetic; antianemic;
 KM neuroprotective; human; ss.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 65..1696
 FT /tag= a
 FT /product= "Human PPRG-10"
 FT sig_peptide 65..139
 FT /tag= b
 FT mat_peptide 140..1693
 FT /tag= c
 FT /product= "Mature PPRG-10"
 FT misc_binding 1190..1234
 FT /tag= d
 FT /bound_moiety= "Probe or Primer"
 FT
 XX
 PN MO200009709-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 06-AUG-1999; 99WO-US017818.
 XX
 PR 10-AUG-1998; 98US-0096114P.
 PR 11-FEB-1999; 99US-0119768P.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Bandman O, Hillman JL, Baughn MR, Azimzai Y, Guegler KJ;
 PI Corley NC, Yue H, Tang YT, Reddy R, Patterson C, Au-Young J;
 PI Shih LL, Lu DM;
 DR WPI; 2000-224346/19.
 DR P-PSDB; AAY70016.
 XX
 PT New human proteases, useful for diagnosis, treatment and prevention of
 PT cell proliferative disorders such as atherosclerosis.
 PS
 XX
 PS Claim 9; Page 106; 114pp; English.
 XX
 CC The present sequence is a cDNA identified in Incyte clone 1393101 derived
 CC from THRN003 cDNA library. It encodes human protease and associated
 CC protein-10 (PPRG-10), which is expressed in reproductive, endocrine,
 CC haematopoietic and immune tissues. Anti-PPRG antibodies can be used as
 CC therapeutic antagonists, reagents for diagnosis and monitoring diseases
 CC and for isolating PPRG. PPRG nucleotide sequence can be used as probe or
 CC primer for diagnosis and monitoring of PPRG-related diseases and gene
 CC mapping. PPRG can be used in the treatment of cell proliferative
 CC disorders like cancer, arteriosclerosis, atherosclerosis, bursitis,
 CC cirrhosis and hepatitis, and immune disorders like AIDS, Addison's
 CC disease, adult respiratory distress syndrome, allergies, ankylosing
 CC spondylitis and amyloidosis
 CC
 SO Sequence 1912 BP; 455 A; 567 C; 487 G; 403 T; 0 U; 0 Other;
 Query Match 91.8%; Score 1742; DB 3; Length 1912;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1892; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GTTAGAGGGGGCTTGTGTCACGAGGAGCGGGGAGATCTTCGGGCATGAGAGCA 60
 DB 17 GTTAGAGGGGGCTTGTGTCACGAGGAGCGGGGAGATCTTCGGGCATGAGAGCA 76
 QY 61 GCGGCTGCTCTCTCCCTCACTCTGAGGTGCTCTGCTCTGCACTGCGCA 120
 DB 77 GCGGCTGCTCTCTCCCTCACTCTGAGGTGCTCTGCTCTGCACTGCGCA 136
 QY 121 GCCCAGATTGCACTGAGGCGCCCACTGCAAGGAGCCCTCTCTCTCAAGTAAGAA 180
 DB 137 GCCCAGATTGCACTGAGGCGCCCACTGCAAGGAGCCCTCTCTCTCAAGTAAGAA 196

QY 181 CGCTTCTCCCACTGCTGACTCCAACTGGAAGGCAAGACTACCTGCTCCGTCGA 240
 DB 197 CGCTTCTCCCACTGCTGACTCCAACTGGAAGGCAAGACTACCTGCTCCGTCGA 256
 QY 241 ACCCAGGCTGCGGGAATCCCACTGCTGCTGAGCAATATGAAAACACGCTTA 300
 DB 257 ACCCAGGCTGCGGGAATCCCACTGCTGCTGAGCAATATGAAAACACGCTTA 316
 QY 301 GTGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 DB 317 GTGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 376
 QY 361 CAGTTCACTCACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 DB 377 CAGTTCACTCACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 436
 QY 421 CAGCAGTCTCTATTTCTCTCACTCACTCACTCACTCACTCACTCACTCACTCA 480
 DB 437 CAGCAGTCTCTATTTCTCTCACTCACTCACTCACTCACTCACTCACTCACTCA 496
 QY 481 TCACCCACAGAGTACCTCCCATCTCACTCACTCACTCACTCACTCACTCACTCA 540
 DB 497 TCACCCACAGAGTACCTCCCATCTCACTCACTCACTCACTCACTCACTCACTCA 556
 QY 541 TTCAGGCTTGGCTGAGAGGCTCAGCAAGTGAAGAGCTCTCAATCTCTCTTG 600
 DB 557 TTCAGGCTTGGCTGAGAGGCTCAGCAAGTGAAGAGCTCTCAATCTCTCTTG 616
 QY 601 TCCCTGGAGGCGCAGAGCAAGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 660
 DB 617 TCCCTGGAGGCGCAGAGCAAGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 676
 QY 661 CAGAGCGGCAACAAGAACCAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 DB 677 CAGAGCGGCAACAAGAACCAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 736
 QY 721 GAACAG 780
 DB 737 GAACAG 796
 QY 781 GTGCTCAGCTGAGACAGACTGAGAGCCAGTTTCACTGTAATCTTATCTTAC 840
 DB 797 GTGCTCAGCTGAGACAGACTGAGAGCCAGTTTCACTGTAATCTTATCTTAC 856
 QY 841 CTTTCTCTTTTGTCTCCCGGATACAGAGTGAAGTCTCTCTATGATATGAGAAC 900
 DB 857 CTTTCTCTTTTGTCTCCCGGATACAGAGTGAAGTCTCTCTATGATATGAGAAC 916
 QY 901 ATCCAGAGGCTCATTCGATCAGCCCAAGAAATGATGAATGAATATATATGATAG 960
 DB 917 ATCCAGAGGCTCATTCGATCAGCCCAAGAAATGATGAATGAATATATATGATAG 976
 QY 961 AACTCTACTGAGAAACCAAAACCTGAGGCTTCTGAGCTGCCCAACAGAGGCC 1020
 DB 977 AACTCTACTGAGAAACCAAAACCTGAGGCTTCTGAGCTGCCCAACAGAGGCC 1036
 QY 1021 TTGCTGTGCTGTGCTATTTGATCTGTGAGAAATATCTGATATACCCCAAGCCAG 1080
 DB 1037 TTGCTGTGCTGTGCTATTTGATCTGTGAGAAATATCTGATATACCCCAAGCCAG 1096
 QY 1081 GCGTGAAGTACATGAGAGAGAGATCTGTTTGGGAAAGTCTGCTGACAGCCTT 1140
 DB 1097 GCGTGAAGTACATGAGAGAGAGATCTGTTTGGGAAAGTCTGCTGACAGCCTT 1156
 QY 1141 GGGGCGGACACATGCTTACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
 DB 1157 GGGGCGGACACATGCTTACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1216
 QY 1201 TGGCACTCAGAGGCGGCTGAGCGGCAACATGAGACACTTCCCAAGAGCTCCCTTT 1260
 DB 1217 TGGCACTCAGAGGCGGCTGAGCGGCAACATGAGACACTTCCCAAGAGCTCCCTTT 1276

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QY 1261 GTGAGCCCTTCTGCTCCAGAGCCGTCATCCGAGCAAGGTTAGGTTCCCGAGAA 1320
DB 1277 GTGAGCCCTTCTGCTCCAGAGCCGTCATCCGAGCAAGGTTAGGTTCCCGAGAA 1336
QY 1321 TCAGGCGCTTTTACGGGCTGAGTTTGTACGGTGGGCTCCAGATGAGCTTCTGGTGGC 1380
DB 1337 TCAGGCGCTTTTACGGGCTGAGTTTGTACGGTGGGCTCCAGATGAGCTTCTGGTGGC 1396
QY 1381 CGGCTTGCACGAAAGGCTGTGAAGATGTCGAGATCTTCTGGTGGCTCCAGATGAGTTCC 1440
DB 1397 CGGCTTGCACGAAAGGCTGTGAAGATGTCGAGATCTTCTGGTGGCTCCAGATGAGTTCC 1456
QY 1441 CTGAGCTTCCAGATGGGAGATTTCTCTACCAAGATTTGTGACACAGACTATATCCAGTAC 1500
DB 1457 CTGAGCTTCCAGATGGGAGATTTCTCTACCAAGATTTGTGACACAGACTATATCCAGTAC 1516
QY 1501 CCAAACTACTGTTCTCTCAAAAGGCAAGCTGTCTGATGAAACCGCAATCGGAAGGTG 1560
DB 1517 CCAAACTACTGTTCTCTCAAAAGGCAAGCTGTCTGATGAAACCGCAATCGGAAGGTG 1576
QY 1561 TCCCGCATGAGATGTCTGCAAGATGAGACTTACAGTGGCTGAGCCCTTGGCAAAAGTGA 1620
DB 1577 TCCCGCATGAGATGTCTGCAAGATGAGACTTACAGTGGCTGAGCCCTTGGCAAAAGTGA 1636
QY 1621 GAGCTTGTGCTGATGAGAGGAGGAGTTCAGAGACTTGTGAGCCAGTTCCGAGTGA 1680
DB 1637 GAGCTTGTGCTGATGAGAGGAGTTCAGAGACTTGTGAGCCAGTTCCGAGTGA 1696
QY 1681 GCTGGGCTTATTTCTGCCACACCCGAGCCCAACCTGCTCTCATTTGTTTGA 1740
DB 1697 GCTGGGCTTATTTCTGCCACACCCGAGCCCAACCTGCTCTCATTTGTTTGA 1756
QY 1741 ACCCCATGCTTTCAGGCTGCTGCTTCTGAGTCTGAGTCTGAGCCCTTCACTCAATTTCC 1800
DB 1757 ACCCCATGCTTTCAGGCTGCTGCTTCTGAGTCTGAGTCTGAGCCCTTCACTCAATTTCC 1816
QY 1801 TTGGGTTGAGCAACAGTCCGAGAGAGGCGCAGTGGGAGCTGGCCCTTAAAGAA 1860
DB 1817 TTGGGTTGAGCAACAGTCCGAGAGAGGCGCAGTGGGAGCTGGCCCTTAAAGAA 1876
QY 1861 TGACTTTACATTAATGTTGATCTTCAAAAAA 1895
DB 1877 TGACTTTACATTAATGTTGATCTTCAAAAAA 1911

RESULT 4
AAK06785
ID AAK06785 standard; cDNA; 1899 BP.
AC AAK06785;
XX
DT 26-APR-1999 (first entry)
DE Human adult testis secreted protein ga63_6 cDNA.
KW Secreted protein; human; testis; ga63_6; ds.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 43..1674
FT FT /tag= a
FT FT /note= "this region (minus the stop codon at 1672..1674)
FT FT is specifically claimed in Claim 24(b)"
FT FT sig_peptide 73..111
FT FT /tag= b
FT FT /product= "putative leader/signal sequence, or
FT FT transmembrane region"
FT FT 112..1671
FT FT /tag= c
FT FT /note= "this region is specifically claimed in Claim
FT FT 24(c)"
FT misc_feature 224..679

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FT FT /tag= d
FT FT /note= "this region is specifically claimed in Claim
FT FT 24(d)"
PN W09857976-A1.
PD 23-DEC-1998.
XX 18-JUN-1998; 98WO-US012516.
PF 19-JUN-1997; 97US-00878715.
PR 17-JUN-1998; 98US-00098588.
XX (GENY) GENETICS INST INC.
PA
PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Treacy M, Spaulding V;
PI Agostino MJ, Howes SH, Fecthel K;
XX WPI; 1999-095321/08.
DR P-PSDB; AAW88403.
XX
PS Claim 24(a); Page 84-85; 122pp; English.
CC This cDNA clone, termed ga63_6, codes for a novel human secreted protein
CC (see AAW88403). The full-length clone was isolated from a human adult
CC testis cDNA library using methods which are selective for cDNAs encoding
CC secreted proteins, or was identified as encoding a secreted or
CC transmembrane protein on the basis of computer analysis of the amino acid
CC sequence of the encoded protein. Its sequence shows at least some
CC similarity to some known database sequences. The invention provides cDNA
CC clones (see AAK06780-89) from human adult testis, foetal brain, adult
CC uterus, adult trachea and adult neural tissue that encode novel secreted
CC proteins (see AAW88398-407). The clones are deposited as ATCC 98468, from
CC which each can be isolated using specified probes (see AAK06790-99). The
CC polynucleotides and proteins are predicted to have biological activities
CC which would make them suitable for treating, preventing or ameliorating
CC medical conditions in humans and animals, although no supporting data is
CC given. Suggested activities include nutritional, cytokine, cell
CC proliferation/differentiation, immune stimulating (e.g. as vaccines) or
CC suppressing, haematopoiesis regulation, tissue growth, activin or
CC inhibin, chemotactic or chemokinetic, haemostatic, thrombolytic activity,
CC receptor/ligand, antiinflammatory, cadherin/tumour invasion suppressor,
CC and tumour inhibition activities. The polynucleotides are also stated to
CC be useful for gene therapy, and for recombinant production of the claimed
CC proteins
CC
SQ Sequence 1899 BP; 457 A; 560 C; 477 G; 401 T; 0 U; 4 Other;
QY Query Match 78.8%; Score 1494; DB 2; Length 1899;
DB Best Local Similarity 99.9%; Pred. No. 0;
Matches 1594; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 11 GCTTGTGTCACGGAACGGGCGGATCTTCTCGGCCATGAGAAAGCAGCCGTGGCT 70
DB 5 GCTTGTGTCACGGAACGGGCGGATCTTCTCGGCCATGAGAAAGCAGCCGTGGCT 64
QY 71 TCCCTCCATCACTCCGAAAGGCTGCTCTGCTTGTGGCACTGCGCAGCCAGATT 130
DB 65 TCCCTCCATCACTCCGAAAGGCTGCTCTGCTTGTGGCACTGCGCAGCCAGATT 124
QY 131 CGACTGAGCCGCCCACTCCAGCAGCCCTCTCTCCCTACCGAATAGAAAGCTTTTGG 190
DB 125 CGACTGAGCCCTCCACTCCAGCAGCCCTCTCTCTCCCTACCGAATAGAAAGCTTTTGG 184
QY 191 CACTGTGACTCCCACTCCGAAAGGAGAGACTTACCTGCTTCCGTGCAACCAAGGCT 250
DB 185 CACTGTGACTCCCACTCCGAAAGGAGAGACTTACCTGCTTCCGTGCAACCAAGGCT 244
QY 251 GCCGGAATCCCACTGCTCAGCTGAGCAATATGAAAACAGAGGCTTAGTCCGAGT 310

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Db 245 GCGGAAATCCACAACCTGCTCAGCTGAGCAAAATGAAAAACAAGGCTTATGTCCTCATG 304
Qy 311 GTGCTGTCTGCTCAACCTGCTTATGCTCTGCTTGTGAGCTTTTGTGCACTTCTACTC 370
Db 305 GTGCTGTCTGCTCAACCTGCTTATGCTCTGCTTGTGAGCTTTTGTGCACTTCTACTC 364
Qy 371 ACTACGGTGTCTCAACCAAGCTTACTATGCAAGAGAGTCTGTGTTTCCCAAGCACTT 430
Db 365 ACTACGGTGTCTCAACCAAGCTTACTATGCAAGAGAGTCTGTGTTTCCCAAGCACTT 424
Qy 431 CTAATTTCTCACTTAACCTTCAAGAGATAGAGAGTCTGAGTCTGAGTCTCAACCA 490
Db 425 CTAATTTCTCACTTAACCTTCAAGAGATAGAGAGTCTGAGTCTGAGTCTCAACCA 484
Qy 491 CGATGACCTTCCCATCTCAACCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 550
Db 485 CGATGACCTTCCCATCTCAACCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 544
Qy 551 GGCCTGAGAGGCTCAGCAACCAAGTGAAGAGCTCTCAATCTCTGCTGCTGAGAG 610
Db 545 GGCCTGAGAGGCTCAGCAACCAAGTGAAGAGCTCTCAATCTCTGCTGCTGAGAG 604
Qy 611 GCCAG 670
Db 605 GCCAG 664
Qy 671 CACAAGAACACAG 730
Db 665 CACAAGAACACAG 724
Qy 731 AG 790
Db 725 AG 784
Qy 791 TGCAGACACACTCAG 850
Db 785 TGCAGACACACTCAG 844
Qy 851 TTGCTCCCCGGGATCAG 910
Db 845 TTGCTCCCCGGGATCAG 904
Qy 911 TCATTGATCAG 970
Db 905 TCATTGATCAG 964
Qy 971 GGAAGAAACCAAAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1030
Db 965 GGAAGAAACCAAAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1024
Qy 1031 TGTGCTATTCGATCGAG 1090
Db 1025 TGTGCTATTCGATCGAG 1084
Qy 1091 ACATGAG 1150
Db 1085 ACATGAG 1144
Qy 1151 ACATGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1210
Db 1145 ACATGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1204
Qy 1211 AGGCGAG 1270
Db 1205 AGGCGAG 1264
Qy 1271 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1330
Db 1265 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1324
Qy 1331 TTTACGGGCTGAGATTTGTACGAGTGGCTCCACATGAGCTTGTGCTGCTGCTGCTGCT 1390

Db 1325 TTTACGGGCTGAGATTTGTACGAGTGGCTCCACATGAGCTTGTGCTGCTGCTGCTGCT 1384
Qy 1391 CGAAGAGCTGTGAAGATGTCGAGTCTGTGGTGGCTCCAGACTGAGTCTTACTGCTCC 1450
Db 1385 CGAAGAGCTGTGAAGATGTCGAGTCTGTGGTGGCTCCAGACTGAGTCTTACTGCTCC 1444
Qy 1451 AGGATGGGAGTTTTCCTTCAACAGATTTGTGACACAGACTATATTCAGTACCCAACTACT 1510
Db 1445 AGGATGGGAGTTTTCCTTCAACAGATTTGTGACACAGACTATATTCAGTACCCAACTACT 1504
Qy 1511 GTTCCTTCAAAACCGAGAGAGTCTGATGAGAAACCGCAATCCGAGAGTGTCCCGCATGA 1570
Db 1505 GTTCCTTCAAAACCGAGAGAGTCTGATGAGAAACCGCAATCCGAGAGTGTCCCGCATGA 1564
Qy 1571 GATGCTGAGATGAGATTTACAGTGGCTGAGCC 1606
Db 1565 GATGCTGAGATGAGATTTACAGTGGCTGAGCC 1600

RESULT 5
AAZ24890
ID AAZ24890 standard; DNA; 1892 BP.
XX
AC AAZ24890;
XX
DT 02-DEC-1999 (first entry)
XX
DE Human secreted protein gene 80 clone HUMAY54.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; aschima; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; revascularisation; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; leucitis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS Homo sapiens.
XX
PN WO947540-A1.
XX
PD 23-SEP-1999.
XX
PF 18-MAR-1999; 99MO-US005804.
XX
PR 19-MAR-1998; 98US-0078563P.
PR 19-MAR-1998; 98US-0078566P.
PR 19-MAR-1998; 98US-0078573P.
PR 19-MAR-1998; 98US-0078576P.
PR 19-MAR-1998; 98US-0078577P.
PR 19-MAR-1998; 98US-0078578P.
PR 19-MAR-1998; 98US-0078579P.
PR 19-MAR-1998; 98US-0078581P.
PR 01-APR-1998; 98US-0080312P.
PR 01-APR-1998; 98US-0080313P.
PR 01-APR-1998; 98US-0080314P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Ni J, Rosen CA, Yu G, Young PE, Feng P, Soppet DR;
PI Wei Y, Endress GA, Duan RD, Kyaw H, Bener R, Lafleur DW, Olsen HS;
PI Shi Y, Moore PA;
XX
DR MPI, 1999-562050/47.
XX
PT P-PSDB; AAY41387.
XX
PT New isolated human genes, useful for diagnosis and treatment of e.g.
PT cancers, neurological disorders, immune diseases, inflammation or blood
PT disorders.
XX
PS Claim 1; Page 346; 484pp; English.

XX AC ADA39940;
 XX DT 20-NOV-2003 (first entry)
 XX DE Human secreted protein encoding cDNA.
 XX KW Human; secreted protein; cancer; hyperproliferative disorder;
 KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
 KW anaemia; allergic reaction; asthma; cardiovascular disorder;
 KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
 KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
 KW vllnerary; cardiant; gene therapy; ss.
 XX OS Homo sapiens.
 XX PN WO2002102993-A2.
 XX PD 27-DEC-2002.
 XX PF 19-MAR-2002; 2002WO-US008123.
 XX PR 21-MAR-2001; 2001US-0277340P.
 XX PR 19-JUL-2001; 2001US-0306171P.
 XX PR 13-NOV-2001; 2001US-0331287P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Ruben SM;
 XX WPI; 2003-175238/17.
 XX DR
 XX XX
 PT PT New human secreted proteins and nucleic acid molecules, useful for
 PT preparing a diagnostic or pharmaceutical composition for diagnosing,
 PT preventing or treating cancer or other hyperproliferative disorder,
 PT asthma, allergies or AIDS.
 PT
 XX
 PS Claim 9; SEQ ID NO 322; 3205pp; English.
 XX
 CC The invention relates to novel genes ADA39629-ADA40565 and proteins
 CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
 CC treating or ameliorating medical conditions e.g. by protein or gene
 CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
 CC fragments, and agonists or antagonists that bind to the polypeptide are
 CC useful for preparing a diagnostic or pharmaceutical composition for
 CC diagnosing or treating cancer or other hyperproliferative disorder. The
 CC polypeptides and nucleic acid molecules are also useful for detecting,
 CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
 CC or other hyperproliferative disorders including neoplasms, autoimmune
 CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
 CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
 CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
 CC thrombocytopenia), allergic reactions including asthma or eczema,
 CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
 CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
 CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
 CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
 CC fungal or viral infections including HIV/AIDS), or wound healing and
 CC disorders of epithelial cell proliferation. The nucleic acids are also
 CC useful for chromosome identification, radiation hybrid mapping or long-
 CC range restriction mapping, as molecular weight markers, or as
 CC hybridization or diagnostic probes. The polypeptides and antibodies are
 CC useful for providing immunological probes for differential identification
 CC of the tissues immunohistochemistry assays. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pat_sequences.
 CC
 CC Sequence 1892 BP; 461 A; 565 C; 472 G; 394 T; 0 U; 0 Other;
 CC
 CC Query Match 67.8%; Score 1284; DB 8; Length 1892;
 CC Best Local Similarity 99.7%; Pred. No. 0;
 CC Matches 1794; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

Qy	33	CGGATCTTCTCCGGCCATGAGAAAGCCAGCGGTGCTTCTTCCCTCACTCTGAAGT	92
Db	22	CGGATCTTCTCCGGCCATGAGAAAGCCAGCGGTGCTTCTTCCCTCACTCTGAAGT	81
Qy	93	GCTGCTCTGCTCTTGACCTTGCGACCTTGCGACCTTGCGACCTTGCGACCTTGCGAC	152
Db	82	GCTGCTCTGCTCTTGACCTTGCGACCTTGCGACCTTGCGACCTTGCGACCTTGCGAC	141
Qy	153	CAGCCCTCTCTCTTCCGAAATGAGAAAGCTTCTTGCACTGCTGCTCAACTGGA	212
Db	142	CAGCCCTCTCTCTTCCGAAATGAGAAAGCTTCTTGCACTGCTGCTCAACTGGA	201
Qy	213	GGGAGAGACTACCTGCGCTCTGCGCAACCCAGCGTGGCGGAATCCACACTGTC	272
Db	202	GGGAGAGACTACCTGCGCTCTGCGCAACCCAGCGTGGCGGAATCCACACTGTC	261
Qy	273	GCTGGAACCAATATGAAAAACAGGCTTATGTCCTGATGCTGCTGCTGCTGCTGCTG	332
Db	262	GCTGGAACCAATATGAAAAACAGGCTTATGTCCTGATGCTGCTGCTGCTGCTGCTG	321
Qy	333	TTATGCTCTCTGCTTGAAGCTTCTTGCGCACTTCACTACCTTGCTCCAACTGCT	392
Db	322	TTATGCTCTCTGCTTGAAGCTTCTTGCGCACTTCACTACCTTGCTCCAACTGCT	381
Qy	393	CTACTATGCAAGAGAGTCTGCTGCTTCCAGCGAGTCTCACTTCTCACTCACTCT	452
Db	382	CTACTATGCAAGAGAGTCTGCTGCTTCCAGCGAGTCTCACTTCTCACTCACTCT	441
Qy	453	CAAGAGATTAAGAGCTTCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	512
Db	442	CAAGAGATTAAGAGCTTCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	501
Qy	513	CCACTTCAAGTACAGAAAGCCAGACCTTCCAGCTTCCAGCTTCCAGCTTCCAGCA	572
Db	502	CCACTTCAAGTACAGAAAGCCAGACCTTCCAGCTTCCAGCTTCCAGCTTCCAGCA	561
Qy	573	CGTGAAGAGCTCTCAATCTCTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	632
Db	562	CGTGAAGAGCTCTCAATCTCTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	621
Qy	633	CAAGCAGAGCAAGAGTGGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAG	692
Db	622	CAAGCAGAGCAAGAGTGGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAG	681
Qy	693	GGGCGCAAAACAGAAAGAGCAAGAAAGCAAGAAAGCAAGAAAGCAAGAAAGCAAG	752
Db	682	GGGCGCAAAACAGAAAGAGCAAGAAAGCAAGAAAGCAAGAAAGCAAGAAAGCAAG	741
Qy	753	ACAGGGGAACTAAGAGAGGAGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG	812
Db	742	ACAGGGGAACTAAGAGAGGAGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG	801
Qy	813	GTTTCACTGATCTCTATCTTCTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	872
Db	802	GTTTCACTGATCTCTATCTTCTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	861
Qy	873	AGAGTCTACTCTATATATATGAGAAATCCAGAGCTCATTCGATCAGCCAGAAAT	932
Db	862	AGAGTCTACTCTATATATATGAGAAATCCAGAGCTCATTCGATCAGCCAGAAAT	921
Qy	933	AGATGAATGAATGAATATATATGAGAAATCTCTCTGAGAAACCAAAACCTGGCAG	992
Db	922	AGATGAATGAATGAATATATATGAGAAATCTCTCTGAGAAACCAAAACCTGGCAG	981
Qy	993	CTTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1052
Db	982	CTTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1040
Qy	1053	TACTTGATCATTAACCCCAAGCCCAAGGCTTGAAGTATATGAGAGAGAGATCTTGG	1112
Db	1041	TACTTGATCATTAACCCCAAGGCTTGAAGTATATGAGAGAGAGATCTTGG	1100

CC identification, radiation hybrid mapping or long-range restriction
 CC mapping, as molecular weight markers or as hybridization or diagnostic
 CC probes. The polypeptides and antibodies are useful for providing
 CC immunological probes for differential identification of the tissues
 CC immunohistochemistry assays. The present sequence represents a human
 CC secreted protein encoding sequence.

XX Sequence 1892 BP; 461 A; 565 C; 472 G; 394 T; 0 U; 0 Other;

Query Match 67.8%; Score 1284; DB 10; Length 1892;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1794; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

```

Qy 33 CGGATCTTCTCCGCCATGAGAAAGCCAGCCGCTGCTCTCTCCCTCACTCTGAAAGT 92
Db 22 CGGATCTTCTCCGCCATGAGAAAGCCAGCCGCTGCTCTCTCCCTCACTCTGAAAGT 81
Qy 93 GCTGCTCTGCTCTGACACCTGCGGAGCCGAGATTGACTCAGAGCCCACTCCAG 152
Db 82 GCTGCTCTGCTCTGACACCTGCGGAGCCGAGATTGACTCAGAGCCCACTCCAG 141
Qy 153 CAGCCCTCTCTCTCTACCGAATACGACCTTCTGCACTGCTGACTCCCACTCCAG 212
Db 142 CAGCCCTCTCTCTCTACCGAATACGACCTTCTGCACTGCTGACTCCCACTCCAG 201
Qy 213 GGCAGAGACTACCTGCGCTGCTGCGACACCAAGCTGCGGAATCCCACTCCAG 272
Db 202 GGCAGAGACTACCTGCGCTGCTGCGACACCAAGCTGCGGAATCCCACTCCAG 261
Qy 273 GCTGAGCAATATGAAACCAAGCTTAACTGACCGATGATGCTGCTGCTCCCACTCC 332
Db 262 GCTGAGCAATATGAAACCAAGCTTAACTGACCGATGATGCTGCTGCTCCCACTCC 321
Qy 333 TTATGCTCTCTGTTGAGTCTTCTGCAAGTTCCTACTACCTGCTCCCACTCC 392
Db 322 TTATGCTCTCTGTTGAGTCTTCTGCAAGTTCCTACTACCTGCTCCCACTCC 381
Qy 393 CTACTATGCGAAGAGTCTGCTGCTTCCAGCAGTCTCTATCTCTCACTTAACTCT 452
Db 382 CTACTATGCGAAGAGTCTGCTGCTTCCAGCAGTCTCTATCTCTCACTTAACTCT 441
Qy 453 CAGAGAGATAGAAAGTTCAGCTGAAGTCTCAACCAACGATGACCTCCCACTCC 512
Db 442 CAGAGAGATAGAAAGTTCAGCTGAAGTCTCAACCAACGATGACCTCCCACTCC 501
Qy 513 CCATCTCAAGTACAGAAAGCCAGACCTTCCAGCCTGCTGAGAGGCTCCAGCA 572
Db 502 CCATCTCAAGTACAGAAAGCCAGACCTTCCAGCCTGCTGAGAGGCTCCAGCA 561
Qy 573 CGTGAAGAGTCTCTACCAATCTCTCTGCTGCTGAGAGGCTCCAGAGCA 632
Db 562 CGTGAAGAGTCTCTACCAATCTCTCTGCTGCTGAGAGGCTCCAGAGCA 621
Qy 633 CAACAGAGAGAGAGTGAAGCAAGAGCAGAGCCGACCAAGAAACAACAAGAA 692
Db 622 CAACAGAGAGAGAGTGAAGCAAGAGCAGAGCCGACCAAGAAACAACAAGAA 681
Qy 693 GGGGCAAGAAACAGAAAGAGCAAGAAAGCAAGAAAGAGGAAAGCAAGAAAG 752
Db 682 GGGGCAAGAAACAGAAAGAGCAAGAAAGCAAGAAAGAGGAAAGCAAGAAAG 741
Qy 753 ACAGGGGACTAAGAGAGAGAGGAGGCTGTCTGAGCTGAGAGAGACTCAGAGCC 812
Db 742 ACAGGGGACTAAGAGAGAGAGGAGGCTGTCTGAGCTGAGAGAGACTCAGAGCC 801
Qy 813 GTTCACTCTGAATCTCTATCTTTTAAACCTCTCTCTTCTCCCGGATCAGAAAGT 872
Db 802 GTTCACTCTGAATCTCTATCTTTTAAACCTCTCTCTTCTCCCGGATCAGAAAGT 861
Qy 873 AAGAGTCTACTCTATGATATGAGAAATCAGAGAGCTCATTTGATCAGAGCCGAAAT 932
Db 862 AAGAGTCTACTCTATGATATGAGAAATCAGAGAGCTCATTTGATCAGAGCCGAAAT 921

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Qy 993 AGATGAATGATGAATATATATGAGAACTCTCTAGTGAAGAAACCAAAACCTGGCAG 992
Db 922 AGATGAATGATGAATATATATGAGAACTCTCTAGTGAAGAAACCAAAACCTGGCAG 981
Qy 993 CTTCTCTAGCTGCCCCCAGACAGAGGCTTTCCTGCTGCTGCTGCTGCTGCTGCTG 1052
Db 982 CTTCTCTAGCTGCCCCCAGACAGAGGCTTTCCTGCTGCTGCTGCTGCTGCTGCTG 1040
Qy 1053 TACCTGATATATACCCCAACAGCCAGCTGAGATGATGAGAGAGAGATCTTGG 1112
Db 1041 TACCTGATATATACCCCAACAGCCAGCTGAGATGATGAGAGAGAGATCTTGG 1100
Qy 1113 TTTGAGAGAGTCTGCTGCTGAGAGAGCTTGGAGAGAGAGAGAGAGAGAGAGAG 1172
Db 1101 TTTGAGAGAGTCTGCTGCTGAGAGAGCTTGGAGAGAGAGAGAGAGAGAGAGAG 1160
Qy 1173 TGACTTCTGCTCTTGAAGCTGAGAGAGTCCACTCAGAGAGAGAGAGAGAGAG 1232
Db 1161 TGACTTCTGCTCTTGAAGCTGAGAGAGTCCACTCAGAGAGAGAGAGAGAGAG 1220
Qy 1233 ATGCGACACTTCCCAAGAGACTCCCTTGTGAGAGAGAGAGAGAGAGAGAGAG 1292
Db 1221 ATGCGACACTTCCCAAGAGACTCCCTTGTGAGAGAGAGAGAGAGAGAGAGAG 1279
Qy 1293 CATGGGCAACAGGATGAGGCTCCCAAGATCAGAGAGAGAGAGAGAGAGAGAG 1352
Db 1280 CATGGGCAACAGGATGAGGCTCCCAAGATCAGAGAGAGAGAGAGAGAGAGAG 1339
Qy 1353 TGGGCTCCAGATGAGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1412
Db 1340 TGGGCTCCAGATGAGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1399
Qy 1413 AGTCTCTGAGGCTCCAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1472
Db 1400 AGTCTCTGAGGCTCCAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1458
Qy 1473 GATTGATGACAGACATATATGAGATCCCAATCTACTGCTTCTTCAAAAGCAGAG 1532
Db 1459 GATTGATGACAGACATATATGAGATCCCAATCTACTGCTTCTTCAAAAGCAGAG 1518
Qy 1533 TCTGATGAGAAACCGCAATGAGAGTGTCCGATGAGATGCTGAGAGATGAGACT 1592
Db 1519 TCTGATGAGAAACCGCAATGAGAGTGTCCGATGAGATGCTGAGAGATGAGACT 1578
Qy 1593 CAGTGCCTAGAGCCTGAGCAAAAGTGAAGAGTGTGCTGCTGATGAGAGAGAG 1652
Db 1579 CAGTGCCTAGAGCCTGAGCAAAAGTGAAGAGTGTGCTGCTGATGAGAGAGAG 1638
Qy 1653 CACTTGAAGCTTGAAGCAGTTCGATGAGAGTGGCTGCTGCTGCTGCTGCTGCT 1712
Db 1639 CACTTGAAGCTTGAAGCAGTTCGATGAGAGTGGCTGCTGCTGCTGCTGCTGCT 1698
Qy 1713 ACCTGGCCAGTTCCTATATGTTGAGAGCCCAATGCTTCTGAGAGCTGCTGCT 1772
Db 1699 ACCTGGCCAGTTCCTATATGTTGAGAGCCCAATGCTTCTGAGAGCTGCTGCT 1758
Qy 1773 CTGTTACTGAGCCTTACTCAATTTCTTGGGTTGAGAGCAAGTCCAGAGAGGCC 1832
Db 1759 CTGTTACTGAGCCTTACTCAATTTCTTGGGTTGAGAGCAAGTCCAGAGAGGCC 1818

```

RESULT 9
 ADA56130
 ID ADA56130 standard; DNA; 1892 BP.

AC ADA56130;

DT 20-NOV-2003 (first entry)

XX Gene encoding human secreted protein #309.

DE immunosuppressive; antiinflammatory; antilethemic; antiallergic;
 XX cytostatic; cerebroprotective; neuroprotective; nootropic;
 KW

Db 697 GTCTACTATGCCAAGAGAGTCTGTGTCCAGCAGCTCTCTATCTCTCACTAAGACT 756
Qy 451 CTCAGAGAGATAGAGCTTCAGCTGAAGTCTCAACCCACAGATGACTCCCATCTCA 510
Db 757 CTCAGAGAGATAGAGCTTCAGCTGAAGTCTCAACCCACAGATGACTCCCATCTCA 816
Qy 511 CCCCACTTCACAGTGAAGAGCCGAGACCTTCCAGCCCTGGCTGAGAGGCTTCAGAAC 570
Db 817 CCCCACTTCACAGTGAAGAGCCGAGACCTTCCAGCCCTGGCTGAGAGGCTTCAGAAC 876
Qy 571 AAGGTGAAGAGCTCTCAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 630
Db 877 AAGGTGAAGAGCTCTCAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 936
Qy 631 CACAGCAGAGAGAGAGAGTGAAGCAGCAGCAGAGAGCCGACACAGAGAACACAGAGAGAA 690
Db 937 CACAGCAGAGAGAGAGAGTGAAGCAGCAGCAGAGAGCCGACACAGAGAACACAGAGAGAA 996
Qy 691 GAGGGGCGAGAAACAGAA 750
Db 997 GAGGGGCGAGAAACAGAA 1056
Qy 751 GAGCAGAGAGAGCTAAG 810
Db 1057 GAGCAGAGAGAGCTAAG 1116
Qy 811 AAGTTCACTCTGAATCTCTATCTCTCAACCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 870
Db 1117 AAGTTCACTCTGAATCTCTATCTCTCAACCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1176
Qy 871 GTAGAGCTTACTCTCTATGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 930
Db 1177 GTAGAGCTTACTCTCTATGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1236
Qy 931 ATAGATGAATATGAAT 990
Db 1237 ATAGATGAATATGAAT 1296
Qy 991 AGCTTCCTGAGCTGAGCCCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1050
Db 1297 AGCTTCCTGAGCTGAGCCCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1356
Qy 1051 AATACCTGATCATTAACCCCAAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1110
Db 1357 AATACCTGATCATTAACCCCAAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1416
Qy 1111 GGTTCGGGAGAGTCCGTCTGTGACAGCTTGGGCGGAGACATGTCTTACTGTGCCCTC 1170
Db 1417 GGTTCGGGAGAGTCCGTCTGTGACAGCTTGGGCGGAGACATGTCTTACTGTGCCCTC 1476
Qy 1171 TGTGACTTTCGCTCTTTGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1230
Db 1477 TGTGACTTTCGCTCTTTGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1536
Qy 1231 CAATGAGACACTCCCAAGAGACTCCCTTGTGACAGCCCTTGTGCTCCAGAGAGCTG 1290
Db 1537 CAATGAGACACTCCCAAGAGACTCCCTTGTGACAGCCCTTGTGCTCCAGAGAGCTG 1596
Qy 1291 TCCATGCGGACCAAG 1350
Db 1597 TCCATGCGGACCAAG 1656
Qy 1351 GGTGGGCTCCAGATG 1365
Db 1657 GGTGGGCTCCAGATG 1671

RESULT 11
ADO24565
ID ADO24565 standard; cDNA; 3306 BP.
AC
XX
ADO24565;
XX

DT 12-AUG-2004 (first entry)
XX
DE Human PRO7347 encoding cDNA SEQ ID NO:204.
XX
KW human; PRO; antiautismic; antiarthritic; antiinflammatory; antipsoriatic;
KW antineutritic; dermatological; immunostimulant; immunosuppressive;
KW osteopathic; vasotropic; immune response; rheumatoid arthritis; osteoarthritis;
KW juvenile chronic arthritis; systemic lupus erythematosus;
KW spondyloarthritis; systemic sclerosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome;
KW systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
KW autoimmune disease; immune-mediated skin disease; bullous skin disease;
KW erythema multiforme; contact dermatitis; psoriasis; lymphadenopathy;
KW splenomegaly; leukopenia; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004043397-A2.
XX
PD 27-MAY-2004.
XX
PF 12-NOV-2003; 2003MO-US036002.
XX
PR 12-NOV-2002; 2002US-0425931P.
XX
PA (GETH) GENENTECH INC.
XX
PI Abbas A, Bodary S, Clark H, Wu TD, Schoenfeld J, Wood WI;
XX
XX WPI; 2004-420080/39.
DR P-FSDB; ADO24566.
XX
PT New isolated PRO polypeptide e.g. PRO37544, PRO69493, PRO87327 etc,
PT capable of stimulating an immune response, useful for treating diseases
PT such as rheumatoid arthritis, psoriasis, and leukopenia.
XX
PS Claim 2; SEQ ID NO 204; 326pp; English.
XX
CC The present invention describes an isolated human PRO polypeptide (I).
CC also described: (1) an isolated PRO nucleic (II) acid encoding (I); (2) a
CC vector (III) comprising (II); (3) a host cell (IV) comprising (II); (4)
CC producing (I); (5) a chimeric molecule (V) comprising (I) fused to a
CC heterologous amino acid sequence; (6) an antibody (VI) which specifically
CC binds to (I); (7) a composition of matter comprising (I), an agonist of
CC (I), an antagonist of (I), or (VI) in combination with a carrier; (8)
CC treating (MI) an immune related disorder in a mammal, by administering
CC (I), an agonist of (I), an antagonist of (I), or the antibody (VI); (9)
CC diagnosing an immune related disease in a mammal, by detecting the level
CC of expression of a gene encoding (I) in a test sample of tissue cells
CC obtained from the mammal and in a control sample of known normal tissue
CC cells of the same cell type; (10) identifying a compound that inhibits
CC the activity of (I); (11) identifying a compound (M2) that inhibits the
CC expression of a gene encoding (I); (12) identifying a compound that
CC mimics the activity of (I); and (12) stimulating the immune response in a
CC mammal, by administering (I) or its antagonist to the mammal. (I) has
CC antineutritic, antiarthritic, antiinflammatory, antipsoriatic,
CC antineutritic, dermatological, immunostimulant, immunosuppressive,
CC osteopathic and vasotropic activities. (I) and (VI) are useful for
CC diagnosing an immune related disease in a mammal. (II) is useful for
CC diagnosing an inflammatory immune response in a mammal. (VI) is useful
CC for determining the presence of (I) in a sample suspected of containing
CC the polypeptide. (MI) is useful for treating mammal having an immune
CC related disorder chosen from rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, systemic lupus erythematosus,
CC spondyloarthritis, systemic sclerosis, idiopathic inflammatory
CC myopathies, Sjogren's syndrome, autoimmune vasculitis, sarcoidosis,
CC autoimmune haemolytic anaemia, autoimmune or immune-mediated skin
CC diseases including bullous skin diseases, erythema multiforme and contact
CC dermatitis, psoriasis, lymphadenopathy, splenomegaly and leukopenia. The
CC present sequence encodes a human PRO protein from the present invention.
XX
SQ Sequence 3306 BP; 737 A; 950 C; 821 G; 746 T; 0 U; 52 Other;

Query Match 28.3%; Score 536; DB 12; Length 3306;
 Best Local Similarity 100.0%; Pred. No. 2.2e-247;
 Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1025 TGTGCTGTGCTATTCGATCGTGAAGAAATACCTGATCATTAACCCCAAGCCCT 1084
 DB 1890 TGTGCTGTGCTATTCGATCGTGAAGAAATACCTGATCATTAACCCCAAGCCCT 1949
 QY 1085 GGAATACATGAGAGAGAGATCTTGTGTTTGGGAAAGTGGTCTGTGACAGCCCTTGGC 1144
 DB 1950 GGAATACATGAGAGAGAGATCTTGTGTTTGGGAAAGTGGTCTGTGACAGCCCTTGGC 2009
 QY 1145 GGGCAACATGTCTACCTGTGCTCTGTGATCTTGTGCTCTGTGAGCTGAGCAATGCC 1204
 DB 2010 GGGCAACATGTCTACCTGTGCTCTGTGATCTTGTGCTCTGTGAGCTGAGCAATGCC 2069
 QY 1205 ACTGAGAGGCGAGCTGAGCAAGGCAACATGAGCACTTCCCAAGACTCCCTTGTCA 1264
 DB 2070 ACTGAGAGGCGAGCTGAGCAAGGCAACATGAGCACTTCCCAAGACTCCCTTGTCA 2129
 QY 1265 GCGCTTGTGCTGCTCCAGAGCTGTGCTCAATGAGCAAGGAGGTGCTCCAGATCAG 1324
 DB 2130 GCGCTTGTGCTGCTCCAGAGCTGTGCTCAATGAGCAAGGAGGTGCTCCAGATCAG 2189
 QY 1325 GCGCTTGTGCTGCTGATTTGTACGTGGGCTCCATGAGCACTTGTGCTGCGCGGC 1384
 DB 2190 GCGCTTGTGCTGCTGATTTGTACGTGGGCTCCATGAGCACTTGTGCTGCGCGGC 2249
 QY 1385 TTGCGACGAAAGGCTGTGAAGATGTCCGAGTCTGCGGGGTGCTCCAGCTGATCTTCA 1444
 DB 2250 TTGCGACGAAAGGCTGTGAAGATGTCCGAGTCTGCGGGGTGCTCCAGCTGATCTTCA 2309
 QY 1445 GCTTCAGAGATGGGATTTCCCTACCAAGATTTGTGACACAGACTATATCCAGTACCAG 1504
 DB 2310 GCTTCAGAGATGGGATTTCCCTACCAAGATTTGTGACACAGACTATATCCAGTACCAG 2369
 QY 1505 ACTACTGTTCCTTCAAAAGCCAGAGTGTGATGAGAAACCGCAATCCGAAAGGTG 1560
 DB 2370 ACTACTGTTCCTTCAAAAGCCAGAGTGTGATGAGAAACCGCAATCCGAAAGGTG 2425

RESULT 12

AAK97739 standard; DNA; 964 BP.
 XX AAK97739;

AC AAK97739;
 XX
 DT 13-SEP-1999. (first entry)
 XX

DE Extended human secreted protein coding sequence, SEQ ID NO. 304.
 XX

KW Secreted protein; human; cytokine; cellular proliferation; cell movement;
 KW cellular differentiation; immune system regulator; anti-inflammatory;
 KW haematopoiesis regulator; tissue growth regulator; tumour inhibitor;
 KW reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
 KW genetic disease; sr.

OS Homo sapiens.
 XX

PN W09931236-A2.
 XX

PD 24-JUN-1999.
 XX

PF 17-DEC-1998; 98MO-IB002122.
 XX

PR 17-DEC-1997; 97US-0069957P.
 PR 09-FEB-1998; 98US-0074121P.
 PR 13-APR-1998; 98US-0081563P.
 PR 10-AUG-1998; 98US-0096116P.
 XX
 PA (BEST) GENSET.
 XX

PI Bouquelier L, Duclert A, Dumas Milne Edwards J;
 XX WPI, 1999-385906/32.
 DR P-PSDB; AAY36055.
 XX

New isolated human secreted proteins.

Claim 1; Page 377; 516pp; English.

This sequence represents an extended human secreted protein coding
 sequence of the invention. The secreted proteins can be used in treating
 or controlling a variety of human conditions. The secreted proteins may
 act as cytokines or may affect cellular proliferation or differentiation
 or may act as immune system regulators, haematopoiesis regulators, tissue
 growth regulators, regulators of reproductive hormones or cell movement
 or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or
 tumour inhibition activity. The DNAs can be used in forensic procedures
 to identify individuals or in diagnostic procedures to identify
 individuals having genetic diseases resulting from abnormal expression of
 the genes corresponding to the extended cDNAs. They are also useful for
 constructing a high resolution map of the human chromosomes. They can
 also be used for gene therapy to control or treat genetic diseases

Sequence 964 BP; 258 A; 294 C; 227 G; 180 T; 0 U; 5 Other;

Query Match 27.9%; Score 528; DB 2; Length 964;
 Best Local Similarity 99.3%; Pred. No. 1.6e-243;
 Matches 948; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 30 GGGCGGATTTCTCCGGCATGAGAGAGCCAGCCGCTTCTTCTTCTCACTCTGAA 89
 DB 2 GGGCGGATTTCTCCGGCATGAGAGAGCCAGCCGCTTCTTCTTCTCACTCTGAA 61
 QY 90 GGTGTGCTCTGCTCTGCTGCACTGCGAGCCAGAGATTGACTAGAGCCCTCC 149
 DB 62 GGTGTGCTCTGCTCTGCTGCACTGCGAGCCAGAGATTGACTAGAGCCCTCC 121
 QY 150 AGGCGCCCTCTCTCTCTGCAATACGAAATGAAAGCTTGTGCACTGCTCAACTG 209
 DB 122 AGGCGCCCTCTCTCTCTGCAATACGAAATGAAAGCTTGTGCACTGCTCAACTG 181
 QY 210 GAAGGAGAGACTACTGCGCTGCGTGAACCGAGTGGCGGAAATCCCACTGCT 269
 DB 182 GAAGGAGAGACTACTGCGCTGCGTGAACCGAGTGGCGGAAATCCCACTGCT 241
 QY 270 CCACTGAGCAATATATAAACAAGCTTATGATGATGATGATGATGATGATGATGAT 329
 DB 242 CCACTGAGCAATATATAAACAAGCTTATGATGATGATGATGATGATGATGATGAT 301
 QY 330 CCTTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 389
 DB 302 CCTTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361
 QY 390 CGTCTACTATGCAAGAGCTCTGTTTCCAGGCAAGTCTATCTCTCACTAAGC 449
 DB 362 CGTCTACTATGCAAGAGCTCTGTTTCCAGGCAAGTCTATCTCTCTCTCAAGC 421
 QY 450 TCTCAAGAGATGAGCTTCACTGAGTCAACCCACAC-GATGACTTCCCATCT 508
 DB 422 TCTCAAGAGATGAGCTTCACTGAGTCAACCCACAC-GATGACTTCCCATCT 481
 QY 509 CACCCCACTTCAAGTGAAGAGCCAGACCTTCCAGCCCTGCTGAGAGGCTCAGCA 568
 DB 482 CACCCCACTTCAAGTGAAGAGCCAGACCTTCCAGCCCTGCTGAGAGGCTCAGCA 541
 QY 569 ACAAGTGAAGAGCTCCCAATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 628
 DB 542 ACAAGTGAAGAGCTCCCAATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
 QY 629 AGCAAGAGAGAGAGAGAGTGAAGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG 688
 DB 602 AGCAAGAGAGAGAGAGAGTGAAGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG 661

RESULT 14
ACH27630
ID ACH27630 standard; cDNA; 469 BP.
XX
XX ACH27630;
AC
XX
XX 13-OCT-2003 (first entry)
DT
XX
XX Human adult ovary cDNA #6010.
DE
XX
XX Human; ss; sequencing by hybridisation; SH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
XX Homo sapiens.
OS
XX
XX US2003073623-A1.
PN
XX
XX 17-APR-2003.
PD
XX
XX 30-JUL-2001; 2001US-00918995.
PF
XX
XX 30-JUL-2001; 2001US-00918995.
PR
XX
XX 30-JUL-2001; 2001US-00918995.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
PI
XX
XX WPI; 2003-615964/58.
DR
XX
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
XX
XX Claim 1; SEQ ID NO 14842; 44pp; English.
PS
XX
XX The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH27630-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docid=20030073623
XX
XX
SQ Sequence 469 BP; 104 A; 135 C; 123 G; 97 T; 0 U; 10 Other;

Query Match 20.0%; Score 379; DB 9; Length 469;
Best Local Similarity 99.8%; Pred. No. 9.6e-172;
Matches 429; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 936 TGAATGATGATATATATATGATGAACTCTCTGAGAAACCAAAACCTGGCGCTT 995
DB 40 TGAATGATGATATATATATGATGAACTCTCTGAGAAACCAAAACCTGGCGCTT 99
QY 996 CTTGCAAGCTCCCAACAGAGGCTTGTGCTGTGCTGTATTCGATGAGAAATAC 1055
DB 100 CTTGCAAGCTCCCAACAGAGGCTTGTGCTGTGCTGTATTCGATGAGAAATAC 159

QY 1056 CTGCATCATTAACCCCAACAGGCTGTGAGATCATGTAGAGAGAGATCTTGTTT 1115
DB 160 CTGCATCATTAACCCCAACAGGCTGTGAGATCATGTAGAGAGAGATCTTGTTT 219
QY 1116 CGGAAAGTGGTGTGTGACAGCCTTGGGCGGCGACACATGTCTACCTGTGCTGTGA 1175
DB 220 CGGAAAGTGGTGTGTGACAGCCTTGGGCGGCGACACATGTCTACCTGTGCTGTGA 279
QY 1176 CTTCTGCTCTTGAAGCTGAGAGGCGACCTCAAGAGGCGACGCGGCAACATG 1235
DB 280 CTTCTGCTCTTGAAGCTGAGAGGCGACCTCAAGAGGCGACGCGGCAACATG 339
QY 1236 CGACACCTCCCAACAGACTCCCTTGTGACGCCCTTGTGCTGCTCCAGAGCTGTCCAT 1295
DB 340 CGACACCTCCCAACAGACTCCCTTGTGACGCCCTTGTGCTGCTCCAGAGCTGTCCAT 399
QY 1296 CGGCAACGAGTGGTGTGACAGCCTTGGGCGGCGACACATGTCTACCTGTGCTGTGA 1355
DB 400 CGGCAACGAGTGGTGTGACAGCCTTGGGCGGCGACACATGTCTACCTGTGCTGTGA 459
QY 1356 GCTCCACATG 1365
DB 460 GCTCCACATG 469

RESULT 15
ABZ72003
ID ABZ72003 standard; cDNA; 516 BP.
XX
XX ABZ72003;
AC
XX
XX 01-APR-2003 (first entry)
DT
XX
XX Human full length insert cDNA clone YP42A04 GenBank AF085884.
DE
XX
XX Human; cancer; stomach cancer; cytostatic; gene; ss.
KW
XX
XX Homo sapiens.
OS
XX
XX WO200283899-A1.
PN
XX
XX 24-OCT-2002.
PD
XX
XX 28-MAR-2002; 2002MO-JP003038.
PF
XX
XX 10-APR-2001; 2001JP-00112039.
PR 21-SEP-2001; 2001JP-00290193.
XX
XX (TAKA-) TAKARA BIO INC.
PA
XX
XX Yoshikawa Y, Okamoto S, Oura T, Mineno J, Asada K, Kato I;
PI Inoue H, Mori M;
PI WPI; 2003-093022/08.
DR
XX
XX Measuring changes in expression of 264 cancer associated genes for
PT detection of stomach cancer and screening of potential anticancer agents.
PT
XX
XX Claim 2; Page; 266pp; Japanese.
PS
XX
XX The invention relates to a method for the detection of cancer in which a
CC change in the expression of 1 or more of 264 specified cancer associated
CC genes, ABZ71694-ABZ71957, or of sequences at least 80% homologous to them
CC in the specimen tissue as compared to normal tissue is observed. The
CC genes are used in detection, diagnosis and treatment of cancer,
CC especially of stomach cancer. The present sequence is that of a cancer
CC associated polynucleotide of the invention. Note: The present sequence
CC was not given in the printed specification but was isolated using the
CC Genbank accession number given in the DE line
XX
XX
SQ Sequence 516 BP; 112 A; 147 C; 139 G; 118 T; 0 U; 0 Other;

Query Match 17.9%; Score 339; DB 8; Length 516;
Best Local Similarity 100.0%; Pred. No. 1.8e-152;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1557	GGTGTCCCGCATATGATGTCTTGCAATGAGACTTACAGTGGCGTGAAGCCCTGGCAAAAG	1616
DB	177	GGTGTCCCGCATGAGATGCTGCAAGATGAGACTTACAGTGGCGTGAAGCCCTGGCAAAAG	236
QY	1617	TGAGGACGTTGCTTGCATGAGAGCCAGAGATTGAGCACCTTGACTAGAGCCAGTTGGG	1676
DB	237	TGAGGACGTTGCTTGCATGAGAGCCAGAGATTGAGCACCTTGACTAGAGCCAGTTGGG	296
QY	1677	ATGAGCTGGGCGTCTATTCTGCCCAACCCCAAGCCCACTGCCACGTTCTATTGTTT	1736
DB	297	ATGAGCTGGGCGTCTATTCTGCCCAACCCCAAGCCCACTGCCACGTTCTATTGTTT	356
QY	1737	TGAGACCCCATTTGCTTCAAGGCTGCCCTTCTGGGTCTGTTACTGGGCCCTTACTCAGAT	1796
DB	357	TGAGACCCCATTTGCTTCAAGGCTGCCCTTCTGGGTCTGTTACTGGGCCCTTACTCAGAT	416
QY	1797	TTCTTGGGTTTGAGCAACAGTCCCAAGAGAGGGCCACGTTGGGAGCTGGGCCCTTAA	1856
DB	417	TTCTTGGGTTTGAGCAACAGTCCCAAGAGAGGGCCACGTTGGGAGCTGGGCCCTTAA	476
QY	1857	AAGATGACTTTACATAAAATGTGATCTTCAAAAAAAA	1895
DB	477	AAGATGACTTTACATAAAATGTGATCTTCAAAAAAAA	515

Search completed: March 7, 2005, 23:21:24
Job time : 1125 secs

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OM nucleic - nucleic search, using sw model

Run on: March 7, 2005, 15:17:16 ; Search time 1099 Seconds
(without alignments)
10231.701 Million cell updates/sec

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Perfect score: 1895
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5401638 seqs, 2966923429 residues

Total number of hits satisfying chosen parameters: 10803276

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications NA:*
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 - 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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 - 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
 - 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
 - 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
 - 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
 - 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
 - 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
 - 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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 - 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1895	100.0	1895	17	US-10-148-641A-23
2	1886	99.5	1886	16	US-10-262-666-41
3	1886	99.5	1886	17	US-10-085-117-53
4	1881.8	99.3	1892	18	US-10-719-993-124
5	1856.4	98.0	1899	10	US-09-748-783-77
6	1811.2	95.6	1892	17	US-09-397-945-90
7	1811.2	95.6	1892	17	US-10-653-595-90
8	1632	86.1	1632	17	US-10-085-117-54
9	1271.8	67.1	1671	17	US-10-296-115-693
10	1128.2	59.5	1840	17	US-10-085-117-50
11	1062.6	56.1	1623	17	US-10-085-117-51
					Sequence 23, Appl
					Sequence 41, Appl
					Sequence 53, Appl
					Sequence 124, Appl
					Sequence 77, Appl
					Sequence 90, Appl
					Sequence 54, Appl
					Sequence 693, Appl
					Sequence 50, Appl
					Sequence 51, Appl

12	937.6	49.5	964	11	US-09-978-360A-262	Sequence 262, App
13	471.8	24.9	21347	18	US-10-719-993-6794	Sequence 6794, Ap
14	471.8	24.9	29346	17	US-10-085-117-52	Sequence 52, Appl
15	433.8	22.9	469	10	US-09-918-995-14842	Sequence 14842, A
16	408.4	21.6	474	10	US-09-918-995-36471	Sequence 36471, A
17	337.2	17.8	522	18	US-10-474-495-12	Sequence 12, Appl
18	332	17.5	28953	18	US-10-719-993-6811	Sequence 6811, Ap
19	329.8	17.4	507	18	US-10-474-495-230	Sequence 230, App
20	328	17.3	24223	18	US-10-719-993-7043	Sequence 7043, Ap
21	282.4	14.9	308	13	US-10-040-739-641	Sequence 641, App
22	275.8	14.6	36211	17	US-10-085-117-49	Sequence 49, Appl
23	200.6	10.6	201	18	US-10-719-993-2295	Sequence 2295, Ap
24	200.6	10.6	201	18	US-10-719-993-2296	Sequence 2296, Ap
25	199	10.5	201	18	US-10-719-993-2297	Sequence 2297, Ap
26	199	10.5	201	18	US-10-719-993-2298	Sequence 2298, Ap
27	154.6	8.2	157	18	US-10-719-993-2294	Sequence 2294, Ap
28	154.6	8.2	201	18	US-10-719-993-15249	Sequence 15249, A
29	154.6	8.2	201	18	US-10-719-993-17827	Sequence 17827, A
30	139.8	7.4	201	18	US-10-719-993-15240	Sequence 15240, A
31	135.4	7.1	201	18	US-10-719-993-15253	Sequence 15253, A
32	126.6	6.7	370	9	US-09-728-445-80	Sequence 80, Appl
33	119.6	6.3	201	18	US-10-719-993-15250	Sequence 15250, A
34	110.6	5.8	201	18	US-10-719-993-15236	Sequence 15236, A
35	95.4	5.0	201	18	US-10-719-993-15238	Sequence 15238, A
36	88.4	4.7	201	18	US-10-719-993-15251	Sequence 15251, A
37	88	4.6	201	18	US-10-719-993-15239	Sequence 15239, A
C 38	75.6	4.0	28796	13	US-10-087-132-1297	Sequence 1297, Ap
C 39	74	3.9	628	16	US-10-029-386-22859	Sequence 22859, A
C 40	73.4	3.9	51259	17	US-10-374-077-209	Sequence 209, App
C 41	72.6	3.8	16442	17	US-10-374-077-208	Sequence 208, App
C 42	71.2	3.8	1926	15	US-10-294-804-3	Sequence 3, Appl
C 43	71.2	3.8	1926	18	US-10-194-046-3	Sequence 3, Appl
C 44	71.2	3.8	8705	15	US-10-291-230-14	Sequence 14, Appl
C 45	71.2	3.8	8705	15	US-10-291-249-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-10-148-641A-23
; Sequence 23, Application US/10148641A
; Publication No. US20040086852A1
; GENERAL INFORMATION:
; APPLICANT: Ono, Toshio and Nakayama, Eiichi
; TITLE OF INVENTION: CANCER ASSOCIATED ANTIGENS AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: L00461.70132.US
; CURRENT APPLICATION NUMBER: US/10/148,641A
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 09/559,013
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 60/168,353
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 1895
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (49) ... (1677)
US-10-148-641A-23

Query Match 100.0%; Score 1895; DB 17; Length 1895;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1895; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTAGAGCGGCTTGTGTCCACGGACGCGGCGGATCTTCTCCGCCATGAGGAGCCA 60
|||||
Db 1 GTTAGAGCGGCTTGTGTCCACGGACGCGGCGGATCTTCTCCGCCATGAGGAGCCA 60
|||||

SOFTWARE: PatentIn version 3.1
SEQ ID NO 41
LENGTH: 1886
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (49)..(1680)
OTHER INFORMATION:
US-10-262-666-41

Query Match 99.5%; Score 1886; DB 16; Length 1886;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1886; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GTAGAGCGGCTGTGTCCCTCAGCGGACGGGGCGGATCTTCTCCGGCCATGAGGAAGCCA	60
DB	1	GTAGAGCGGCTGTGTCCCTCAGCGGACGGGGCGGATCTTCTCCGGCCATGAGGAAGCCA	60
QY	61	GCGCTGGCTTCTTCCCTCAGCTCCCTGAAAGTGTCTCTGCTCTGCGCAGCTGCGCA	120
DB	61	GCGCTGGCTTCTTCCCTCAGCTCCCTGAAAGTGTCTCTGCTCTGCGCAGCTGCGCA	120
QY	121	GCCAGGATTGCACTCAGGCCCCCACTCCAGGAGGAGACTCTCTCTCTACCGAATACGAA	180
DB	121	GCCAGGATTGCACTCAGGCCCCCACTCCAGGAGGAGACTCTCTCTCTACCGAATACGAA	180
QY	181	CGCTTCTCGCACTGTGACTCCAACTCCGAGGAGGAGACTACTGCGGTCTCCGTGCA	240
DB	181	CGCTTCTCGCACTGTGACTCCAACTCCGAGGAGGAGACTACTGCGGTCTCCGTGCA	240
QY	241	ACCCAGGCTGCCGGAATCCCACTCCGAGGAGGAGACTACTGCGGTCTCCGTGCA	300
DB	241	ACCCAGGCTGCCGGAATCCCACTCCGAGGAGGAGACTACTGCGGTCTCCGTGCA	300
QY	301	GTGCGGATGTGCTGTCTGCTCCAACTCCCTTATGCTCTGCTGCTGCTGCTGCTGCTG	360
DB	301	GTGCGGATGTGCTGTCTGCTCCAACTCCCTTATGCTCTGCTGCTGCTGCTGCTGCTG	360
QY	361	CAGTTCACTACCTGCTGCTCCAACTCCCTTATGCTCTGCTGCTGCTGCTGCTGCTG	420
DB	361	CAGTTCACTACCTGCTGCTCCAACTCCCTTATGCTCTGCTGCTGCTGCTGCTGCTG	420
QY	421	CAGCAGCT	480
DB	421	CAGCAGCT	480
QY	481	TCACCCACCACTGACCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	540
DB	481	TCACCCACCACTGACCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	540
QY	541	TTCCAGCCCTGCTGAGAGGCTCAGCAACACGTTGGAAGAGCTCTCAATCTCTCTCTG	600
DB	541	TTCCAGCCCTGCTGAGAGGCTCAGCAACACGTTGGAAGAGCTCTCAATCTCTCTCTG	600
QY	601	TCCCTGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	660
DB	601	TCCCTGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	660
QY	661	CAGGAGCCGACACAGAAACAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	720
DB	661	CAGGAGCCGACACAGAAACAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	720
QY	721	GAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	780
DB	721	GAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	780
QY	781	GTGTCTCAGCTCAGACAGACTCAGAGCCCAAGTTTCACTCTGAATCTCTATCTTCTAAC	840
DB	781	GTGTCTCAGCTCAGACAGACTCAGAGCCCAAGTTTCACTCTGAATCTCTATCTTCTAAC	840
QY	841	CCTTCT	900
DB	841	CCTTCT	900

RESULT 3
US-10-085-117-53

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; Sequence 53, Application US/10085117
; Publication No. US20030233441
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 1886
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-085-117-53

Query Match          99.5%; Score 1886; DB 17; Length 1886;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1886; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGAGCGGCTGTGTGTCACAGGACGCGGGCGGATCTTCTCGGCCATGAGGAAGCCA 60
DB 1 GTTAGAGCGGCTGTGTGTCACAGGACGCGGGCGGATCTTCTCGGCCATGAGGAAGCCA 60

QY 61 GCCGCTGGCTTCCCTTCCCTCACTCCTCAAGGTGCTGCTCTGCGTCTGGCACTGCGCA 120
DB 61 GCCGCTGGCTTCCCTTCCCTCACTCCTCAAGGTGCTGCTCTGCGTCTGGCACTGCGCA 120

QY 121 GCCCAGGATTCGACTCAGGCGCCCACTCCAGGACGCGCTCTCTCTCTACCGAATACGAA 180
DB 121 GCCCAGGATTCGACTCAGGCGCCCACTCCAGGACGCGCTCTCTCTCTACCGAATACGAA 180

QY 181 CGCTCTTCGCACTGCTGACTCMACTGGAAGGAGACTACTGCGGTCTCCGTGCA 240
DB 181 CGCTCTTCGCACTGCTGACTCMACTGGAAGGAGACTACTGCGGTCTCCGTGCA 240

QY 241 ACCCAGCGCTGCCGGAATCCACACTCGTCAGCTGACCAATATGAAGACCAACGCTTA 300
DB 241 ACCCAGCGCTGCCGGAATCCACACTCGTCAGCTGACCAATATGAAGACCAACGCTTA 300

QY 301 GTGCCCATGGTGTGCTGCTCAACTCCCTTATGCTCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 301 GTGCCCATGGTGTGCTGCTCAACTCCCTTATGCTCTGCTGCTGCTGCTGCTGCTGCTG 360

QY 361 CAGTTCACTCACTACCGTGTCTCAACCACTCTACTATGCTGCTGCTGCTGCTGCTGCTG 420
DB 361 CAGTTCACTCACTACCGTGTCTCAACCACTCTACTATGCTGCTGCTGCTGCTGCTGCTG 420

QY 421 CAGCAGTCTCTATTCTCTCACTAACTCTCAAGGAGATGAGCTTCACTGAAATC 480
DB 421 CAGCAGTCTCTATTCTCTCACTAACTCTCAAGGAGATGAGCTTCACTGAAATC 480

QY 481 TCACCCACCAAGATGACTCCCTTCTCACTCACTCACTCACTCACTCACTCACTCACTCA 540
DB 481 TCACCCACCAAGATGACTCCCTTCTCACTCACTCACTCACTCACTCACTCACTCACTCA 540

QY 541 TTCAGCCCTGGCTGAGAGGCTCAGCAACACGTTGGAAGAGCTCTCAATCTCTCTT 600
DB 541 TTCAGCCCTGGCTGAGAGGCTCAGCAACACGTTGGAAGAGCTCTCAATCTCTCTT 600

QY 601 TCCCTGGAGGCCAGAGCAAGCCAGAGCAACAGCAGGAGCAAGAGTGAGCAAGG 660
DB 601 TCCCTGGAGGCCAGAGCAAGCCAGAGCAACAGCAGGAGCAAGAGTGAGCAAGG 660

QY 661 CAGGACCCGACACAGAAACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
DB 661 CAGGACCCGACACAGAAACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720

QY 721 GAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
DB 721 GAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780

721 GAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
781 GTGTCTCAGCTGCAGACAGACTCAGAGCCCAAGTTTCACTCTGAATCTCTATCTTAAAC 840
781 GTGTCTCAGCTGCAGACAGACTCAGAGCCCAAGTTTCACTCTGAATCTCTATCTTAAAC 840
841 CCTTCTCTTTTGTCTCCCGGGTACGAGAGTACTCTCTATGATGATGATGATGATGATGAT 900
841 CCTTCTCTTTTGTCTCCCGGGTACGAGAGTACTCTCTATGATGATGATGATGATGATGAT 900
901 ATCCAGGAGCTCATTCGATCAGCCAGGAAATAGATGAAATGAAATGAAATGATGATGATGAT 960
901 ATCCAGGAGCTCATTCGATCAGCCAGGAAATAGATGAAATGAAATGAAATGATGATGATGAT 960
961 AACTCTACTGAGAAACCAAAACCCCTGGAGCTCTCTGAGCTGCTGAGCTGCTGAGAGGCC 1020
961 AACTCTACTGAGAAACCAAAACCCCTGGAGCTCTCTGAGCTGCTGAGCTGCTGAGAGGCC 1020
1021 TTGCTGGTGTGTCTATTTCGATCGTGAGAAATACCTGTCATATAACCCCAAGCCCAAG 1080
1021 TTGCTGGTGTGTCTATTTCGATCGTGAGAAATACCTGTCATATAACCCCAAGCCCAAG 1080
1081 GCCTGGAGTACATGGAGGAGGAGATCCTTGGTTTCCGGAAGTCTGCTGTGACAGCCTT 1140
1081 GCCTGGAGTACATGGAGGAGGAGATCCTTGGTTTCCGGAAGTCTGCTGTGACAGCCTT 1140
1141 GGGCGGCGACACATGTCTACCTGTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
1141 GGGCGGCGACACATGTCTACCTGTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
1201 TGCCACTCAGAGGCGAGCTGCGAGGCGCAACATGCGACACCTCCCAAGAGCTCCCTTT 1260
1201 TGCCACTCAGAGGCGAGCTGCGAGGCGCAACATGCGACACCTCCCAAGAGCTCCCTTT 1260
1261 GTACGCCCCCTTGTCTGCTCCAGAGCTCTCCATCGGCAACAGCTAGGTTCCCGAGAA 1320
1261 GTACGCCCCCTTGTCTGCTCCAGAGCTCTCCATCGGCAACAGCTAGGTTCCCGAGAA 1320
1321 TCAGGCGCTTTTACCGGCTGGAATTTGTACGCTGGGCTCCACATGAGCTTCTGGTGTGC 1380
1321 TCAGGCGCTTTTACCGGCTGGAATTTGTACGCTGGGCTCCACATGAGCTTCTGGTGTGC 1380
1381 CGGCTTCCACAGAAAGCTGTGAAGATGCTCCAGTCTCTGGGTGCTCCAGACTGATGTT 1440
1381 CGGCTTCCACAGAAAGCTGTGAAGATGCTCCAGTCTCTGGGTGCTCCAGACTGATGTT 1440
1441 CTTAGCTTCCAGATGGGATTTCCCTACCAAGATTTGTGACACAGACTATATCCAGTAC 1500
1441 CTTAGCTTCCAGATGGGATTTCCCTACCAAGATTTGTGACACAGACTATATCCAGTAC 1500
1501 CCAAACTACTGTTCTTCAAAAGCCAGAGTGTCTGATGAGAAACCGCAATCGGAAGTG 1560
1501 CCAAACTACTGTTCTTCAAAAGCCAGAGTGTCTGATGAGAAACCGCAATCGGAAGTG 1560
1561 TCCCGCATGAGATGTCTGCAAGATGAGACTTACAGTGCCTGAGCCCTGCGCAAAAGTGAG 1620
1561 TCCCGCATGAGATGTCTGCAAGATGAGACTTACAGTGCCTGAGCCCTGCGCAAAAGTGAG 1620
1621 GAGCTTGTCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
1621 GAGCTTGTCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
1681 GCTGGCGTCTATTCTGCCCAACCCAGCCCAACCTGCGCCAGCTTCTTATGTTTGGAG 1740
1681 GCTGGCGTCTATTCTGCCCAACCCAGCCCAACCTGCGCCAGCTTCTTATGTTTGGAG 1740
1741 ACCCGATTCCTTTCAGGCTGCCCCCTTCTGGGTCTGTTACTCGGCCCTTCTCACAATTC 1800
1741 ACCCGATTCCTTTCAGGCTGCCCCCTTCTGGGTCTGTTACTCGGCCCTTCTCACAATTC 1800
1801 TTGGGTGAGCAACAGTCCAGAGAGGCGCCAGCTGGAGCTGGCGCTCTCTTAAAGA 1860
1801 TTGGGTGAGCAACAGTCCAGAGAGGCGCCAGCTGGAGCTGGCGCTCTCTTAAAGA 1860
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QY 1861 TGACTTTACATAAAATGTTGATCTTC 1886
Db |||||
1861 TGACTTTACATAAAATGTTGATCTTC 1886
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RESULT 4
US-10-719-993-124
; Sequence 124, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 5342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 1892
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-124

Query Match 99.3%; Score 1881.8; DB 18; Length 1892;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1880; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTAGAGGGCGGCTTGTTGTCACGGGACGGGGCGGATCTTCCGGCCCATGAGGAAGCCA 60
Db |||||
4 GTTAGAGGGCGGCTTGTTGTCACGGGACGGGGCGGATCTTCCGGCCCATGAGGAAGCCA 63
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QY 61 GCGCTGGGCTTCCTCCCTCACTCTCGAAGGTGCTGCTCTGCTCTGGCACTGCGCGCA 120
Db |||||
64 GCGCTGGGCTTCCTCCCTCACTCTCGAAGGTGCTGCTCTGCTCTGGCACTGCGCGCA 123
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QY 121 GCCCAGGATTCGACTCAGGCGCCCTCCAGGCGGCGCTCTCTCTCTACCGAATACGAA 180
Db |||||
124 GCCCAGGATTCGACTCAGGCGGCTCCACTCCAGGCGGCGCTCTCTCTCTACCGAATACGAA 183
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QY 181 CGCTTCTTCGCACTGCTGACTCCAACTCGAAGGCGAGACTACCTGCGCTCTCCGTGCA 240
Db |||||
184 CGCTTCTTCGCACTGCTGACTCCAACTCGAAGGCGAGACTACCTGCGCTCTCCGTGCA 243
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QY 241 ACCACGGTGGCGGAATCCCACTCTGCTCCAGCTGGACCAATATGAAACCAACGGCTTA 300
Db |||||
244 ACCACGGTGGCGGAATCCCACTCTGCTCCAGCTGGACCAATATGAAACCAACGGCTTA 303
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QY 301 GTGCCGATGGTGTCTGCTCTGCTCCAACTCCCTTATGCTCTGCTGCTGCTGCTGCTG 360
Db |||||
304 GTGCCGATGGTGTCTGCTCTGCTCCAACTCCCTTATGCTCTGCTGCTGCTGCTGCTG 363
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QY 361 CAGTTCACCTCAGTACCTGCTCCAACTGCTCTATGCTCCAAAGAGAGTCTGCTGCTCC 420
Db |||||
364 CAGTTCACCTCAGTACCTGCTCCAACTGCTCTATGCTCCAAAGAGAGTCTGCTGCTCC 423
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QY 421 CAGCCAGTCTCTATCTCTCAGCTAACTCTCAAGGAGATGAAAGCTTCAGCTGAAGTC 480
Db |||||
424 CAGCCAGTCTCTATCTCTCAGCTAACTCTCAAGGAGATGAAAGCTTCAGCTGAAGTC 483
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QY 481 TCACCACCAAGATGATCTCCCTCATCTCAGCTGAGAGTCTCTCACTCACTGAGAGAGG 540
Db |||||
484 TCACCACCAAGATGATCTCCCTCATCTCAGCTGAGAGTCTCTCACTCACTGAGAGAGG 543
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QY 541 TTCCAGCCCTGCTGAGAGGCTCAGCAACAGTGGAGAGTCTCTCACTCACTGAGAGAG 600
Db |||||
544 TTCCAGCCCTGCTGAGAGGCTCAGCAACAGTGGAGAGTCTCTCACTCACTGAGAGAG 603
|||

QY 601 TCCCTGGGAGGCGCAGGAGAGGCGCAGAGCAACAGCAGGAGCAAGGAGTGGAGCAGG 660
Db |||||
604 TCCCTGGGAGGCGCAGGAGAGGCGCAGAGCAACAGCAGGAGCAAGGAGTGGAGCAGG 663
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QY 661 CAGGAGCGCACACAGAACACACAGCAGGAGAGGGCGAGAAACAGAGACGAGCAGAGAG 720
Db |||||
664 CAGGAGCGCACACAGAACACACAGCAGGAGAGGGGCGAGAAACAGAGAGCAGAGAG 723
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QY 721 GAACAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGCT 780
Db |||||
724 GAACAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGCT 783
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QY 781 GTGTCTCAGCTGCAGACAGACTCAGAGCCCAAGTTTCACTCTGAACTCTCTATCTTAAAC 840
Db |||||
784 GTGTCTCAGCTGCAGACAGACTCAGAGCCCAAGTTTCACTCTGAACTCTCTATCTTAAAC 843
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QY 841 CTTCTCTCTTTTGTCTCCCGCGGTACGAGAGTAGAGTCTACTCTATGATAATGAGAGAAC 900
Db |||||
844 CTTCTCTCTTTTGTCTCCCGCGGTACGAGAGTAGAGTCTACTCTATGATAATGAGAGAAC 903
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QY 901 ATCCAGGAGCTCATTCGATCAGCCAGGAAATAGATGAAATGAATGAATATATATGATGAG 960
Db |||||
904 ATCCAGGAGCTCATTCGATCAGCCAGGAAATAGATGAAATGAATGAATATATATGATGAG 963
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QY 961 AACTCTCTAGGAGAAACCAAAACCCCTGCGAGCTTCTGAGCTGCCCCACACAGAGGCC 1020
Db |||||
964 AACTCTCTAGGAGAAACCAAAACCCCTGCGAGCTTCTGAGCTGCCCCACACAGAGGCC 1023
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QY 1021 TTGCTGGTCTGCTGCTATTCGATCGTGGAGAAATACCTGCATCATATACCCCCACAGCAAG 1080
Db |||||
1024 TTGCTGGTCTGCTGCTATTCGATCGTGGAGAAATACCTGCATCATATACCCCCACAGCAAG 1083
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QY 1081 GCCTGGAAGTACATGAGGAGGAGAGATCTTGGTTTCGGGAAAGTCGCTGTGTGACGCTTT 1140
Db |||||
1084 GCCTGGAAGTACATGAGGAGGAGAGATCTTGGTTTCGGGAAAGTCGCTGTGTGACGCTTT 1143
|||

QY 1141 GGGCGGCGACACATGCTTACCTTGTGCTCTGTGACTTCTGCTCTTGAAGCTGGAGCAG 1200
Db |||||
1144 GGGCGGCGACACATGCTTACCTTGTGCTCTGTGACTTCTGCTCTTGAAGCTGGAGCAG 1203
|||

QY 1201 TGCCACTCAGAGGCGCAGCTGCGAGGCGCAACAAATGCGACACTCCCAAGAGCTTCCCTTT 1260
Db |||||
1204 TGCCACTCAGAGGCGCAGCTGCGAGGCGCAACAAATGCGACACTCCCAAGAGCTTCCCTTT 1263
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QY 1261 GTGAGCCCTTCTGCTCCAGAGCTGTCCATCGGCAACAGAGTAGGGTCCCCAGAA 1320
Db |||||
1264 GTGAGCCCTTCTGCTCCAGAGCTGTCCATCGGCAACAGAGTAGGGTCCCCAGAA 1323
|||

QY 1321 TCAGGCGCTTTTACGGGCTGAGTTTGAACGGTGGGCTCCACATGAGCTTCTGCTGTGCC 1380
Db |||||
1324 TCAGGCGCTTTTACGGGCTGAGTTTGAACGGTGGGCTCCACATGAGCTTCTGCTGTGCC 1383
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QY 1381 CGGCTTGCCACAAAGGCTGCAAGTGTCCAGTCTCTGGGTGGCTCCAGACTGAGTTTC 1440
Db |||||
1384 CGGCTTGCCACAAAGGCTGCAAGTGTCCAGTCTCTGGGTGGCTCCAGACTGAGTTTC 1443
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QY 1441 CTTAGCTTCCAGAGTGGGATTTCCCTACCAAGATTTGTGACACAGACTATATCCAGTAC 1500
Db |||||
1444 CTTAGCTTCCAGAGTGGGATTTCCCTACCAAGATTTGTGACACAGACTATATCCAGTAC 1503
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QY 1501 CCAAACTACTGTTCTTCAAAAGCCAGCAGTGTCTGATGAGAAACCGCAATCGGAAGGTG 1560
Db |||||
1504 CCAAACTACTGTTCTTCAAAAGCCAGCAGTGTCTGATGAGAAACCGCAATCGGAAGGTG 1563
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QY 1561 TCCCGCATGAGATGCTGCGAAGTGAAGTTCAGTCCGCTGAGCCCTGCGCAAAAGTGGAG 1620
Db |||||
1564 TCCCGCATGAGATGCTGCGAAGTGAAGTTCAGTCCGCTGAGCCCTGCGCAAAAGTGGAG 1623
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QY 1621 GACGTTGTGCTTCGATGGAGCCAGAGTTCAGCACCTTCACTTAGGCGAGTTCGAGATCA 1680
Db |||||
1624 GACGTTGTGCTTCGATGGAGCCAGAGTTCAGCACCTTCACTTAGGCGAGTTCGAGATCA 1683
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QY 1681 GCTGCGCTTATTTCTGCCACACCCAGCCCAACCTGCCACAGTCTCTATTTGTTTGGAG 1740
Db |||||
1684 GCTGCGCTTATTTCTGCCACACCCAGCCCAACCTGCCACAGTCTCTATTTGTTTGGAG 1743
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QY 1741 ACCCCATTGCTTTTACGGCTGCCCTTCTGGGTCTGTTACTCGGCCCTTACTCACATTTCC 1800
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Db 1201 TCAGAGCCAGCCTGAGCGGCAACAATGCGACACCTCCCAAGACTCCCTTTGTGACG 1260
Qy 1267 CCCTTCTTGCCTCCAGAGCCTGTCCATCGGCAACAGTAGGTGCCAGAAATCAGGC 1326
Db 1261 CCCTTCTTGCCTCCAGAGCCTGTCCATCGGCAACAGTAGGTGCCAGAAATCAGGC 1320
Qy 1327 CGCTTTTACGGCTGGATTGTACGGTGGGCTCCACATGAGACTTCTGGTGTGCGCGCTT 1386
Db 1321 CGCTTTTACGGCTGGATTGTACGGTGGGCTCCACATGAGACTTCTGGTGTGCGCGCTT 1380
Qy 1387 GCCACGAAGGCTGTGAAGATGCCAGTCTCTGGTGGCTCCAGACTGAGTTCTTAGC 1446
Db 1381 GCCACGAAGGCTGTGAAGATGCCAGTCTCTGGTGGCTCCAGACTGAGTTCTTAGC 1440
Qy 1447 TTCCAGATGGGATTTCCCTACCAAGATTTGTGACACAGACTATATCCAGTACCCAAAC 1506
Db 1441 TTCCAGATGGGATTTCCCTACCAAGATTTGTGACACAGACTATATCCAGTACCCAAAC 1500
Qy 1507 TACTGTTCCTTCAAAAGCCAGCAGTGTCTGATGAGAAACCGCAATCGGAAGGTGTCCCGC 1566
Db 1501 TACTGTTCCTTCAAAAGCCAGCAGTGTCTGATGAGAAACCGCAATCGGAAGGTGTCCCGC 1560
Qy 1567 ATGAGATGTCTGCAGAAATGAGACTTACAGTGGCTGAGCCCTGGCAAAAGTGCAGGACGTT 1626
Db 1561 ATGAGATGTCTGCAGAAATGAGACTTACAGTGGCTGAG - CCTGGCAAAAGTGCAGGACGTT 1619
Qy 1627 GTGC - TTCCATGGAGCCAGAGTTACGACCTTGACTCTAGGCCAGTTCCGATGAGCTGG 1685
Db 1620 GTGCTTTCATGGAGCCAGAGTTACGACCTTGACTCTAGGCCAGTTCCGATGAGCTKG 1679
Qy 1686 CGTCTATTCTGCCACACCCAGCCCAACCTGCCACAGTTCTCTATTGTTTTGAGACCCC 1745
Db 1680 SGTATTATTTGCCACACCCAGCCCAACCTGCCACAGTTCTCTATTGTTTTGAGACCCC 1739
Qy 1746 ATTGCTTTTCCAGCTGCCCTTCTGGGTCTGTGTTACTCGGCCCTTACTCATTCTTCTGGG 1805
Db 1740 ATTGCTTTTCCAGCTGCCCTTCTGGGTCTGTGTTACTCGGCCCTTACTCATTCTTCTGGG 1799
Qy 1806 TTGGAGCAACAGTCCAGAGAGGCCACCGTGGGAGCTGGCCCTCTTAAAGATGACT 1865
Db 1800 TTGGAGCAACAGTCCAGAGAGGCCACCGTGGGAGCTGGCCCTCTTAAAGATGACT 1859
Qy 1866 TTACATAAAATGTTGATCTTTCAAAAAAAA 1895
Db 1860 TTACATAAAATGTTGATCTTTCAAAAAAAA 1889
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RESULT 6

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US-09-397-945-90
; Sequence 90, Application US/09397945
; Publication No. US20030065139A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1
; CURRENT APPLICATION NUMBER: US/09/397,945
; PRIOR FILING DATE: 1999-09-17
; APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
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; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,581
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,577
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,563
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,313
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 1892
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-397-945-90
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Query Match 95.6%; Score 1811.2; DB 10; Length 1892;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1860; Conservative 0; Mismatches 8; Indels 4; Gaps 4;

Qy 24 GGACGCGGCGGATCTTCTCCGCCCATGAGGAAGCCAGCGCTGGCTTCTTCCCTCACT 83
Db 13 GGACGCGGAGGATCTTCTCCGCCCATGAGGAAGCCAGCGCTGGCTTCTTCCCTCACT 72
Qy 84 CTGAAGGTGCTGCTCTGCTCTGCACTCTGCGCAGCCAGGATTCGATCAGGCCCC 143
Db 73 CTGAAGGTGCTGCTCTGCTCTGCACTCTGCGCAGCCAGGATTCGATCAGGCCCC 132
Qy 144 CACTCCAGGCGGCTCTCTCTACCAATACGAACGCTTCTTCCGCTGCTGCTGCTCC 203
Db 133 CACTCCAGGCGGCTCTCTCTACCAATACGAACGCTTCTTCCGCTGCTGCTGCTCC 192
Qy 204 AACCTGGAAGGAGAGACTTACCTGCGCTCTCGTGCACACCCAGCGTGCAGGATCCAC 263
Db 193 AACCTGGAAGGAGAGACTTACCTGCGCTCTCGTGCACACCCAGCGTGCAGGATCCAC 252
Qy 264 ACTGCTCAGCTGGACCAATATGAAAAACACCGCTTGTGCGCGATGGTGTCTGCTC 323
Db 253 ACTGCTCAGCTGGACCAATATGAAAAACACCGCTTGTGCGCGATGGTGTCTGCTC 312
Qy 324 CAACTCTCCCTATGCTCTGCTGCTTGTGCTTCTGCGAGTTCACTACCTGCTGCTC 383
Db 313 CAACTCTCCCTATGCTCTGCTGCTTGTGCTTCTGCGAGTTCACTACCTGCTGCTC 372
Qy 384 CAACTCTCTACTATGCAAGAGAGTCTGCTGCTTCCAGCGAGTCTCTATTCTCTCACC 443
Db 373 CAACTCTCTACTATGCAAGAGAGTCTGCTGCTTCCAGCGAGTCTCTATTCTCTCACC 432
Qy 444 TAACTCTCTCAAGGAGATAGAGCTTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAG 503
Db 433 TAACTCTCTCAAGGAGATAGAGCTTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAG 492
Qy 504 CATCTCAGCCCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 563
Db 493 CATCTCAGCCCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 552
Qy 564 CAGCAACAACTGGAAGAGTCTCTCAATCTCTCTGCTGCGAGGCGCAGGAGCAAGC 623
Db 553 CAGCAACAACTGGAAGAGTCTCTCAATCTCTCTGCTGCGAGGCGCAGGAGCAAGC 612
Qy 624 GCCAGAGCAGCAGGAGGAGGAGTGGAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGG 683
Db 613 GCCAGAGCAGCAGGAGGAGGAGTGGAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGG 672
Qy 684 GCAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 743
Db 673 GCAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 732
Qy 744 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 803
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Db 733 GGAAGAGGACAGGGGACTAAGAGGAGCGGAGGCTGTGTCTCAGCTGCAGACACTC 792
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Db 793 AGAGCCCAAGTTTCACTCTGAATCTCTATCTTCTAACCCCTTCTCTTTTGTCTCCCGGGT 852
QY 864 ACCGAGAGTAGAGTCTACTCTCTATCTATGATGAGAACATCCAGGAGCTCATTCGATCAGC 923
Db 853 ACCGAGAGTAGAGTCTACTCTCTATGATGAGAACATCCAGGAGCTCATTCGATCAGC 912
QY 924 CCAGGAAATAGATGAATGAATGAATATATGATGAGAACTCTTACTGAGAAACCAAAA 983
Db 913 CCAGGAAATAGATGAATGAATGAATATATGATGAGAACTCTTACTGAGAAACCAAAA 972
QY 984 CCTGCGACGCTTCTGCGAGCTGCCCAACAGAGGCTTGTGTGTGTGTCTATTTCGAT 1043
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QY 1044 COTGAGAAATACCTGCATCATAACCCCAACAGGCTTGGAGTACATGAGGAGGA 1103
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QY 1164 TGCCCTCTGTGACTTCTGCTCTTGAAGCTGGAGCTGCCACTCAGAGGCGAGCTGCA 1223
Db 1152 TGCCCTCTGTGACTTCTGCTCTTGAAGCTGGAGCTGCCACTCAGAGGCGAGCTGCA 1211
QY 1224 GCGGCAACAATGCGACACCTCCCAAGAGTCTCTTGTGAGCCCTTGTCTGCCCTCCCA 1283
Db 1212 GCGGCAACAATGCGACACCTCCCAAGAGTCTCTTGTGAGCCCTTGTCTGCCCTCCCA 1270
QY 1284 GAGCTGTGCTTCCATCGGCAACAGGTAGGCTGCCAGATCAGGCGGCTTTTACGGGTGGA 1343
Db 1271 GAGCTGTGCTTCCATCGGCAACAGGTAGGCTGCCAGATCAGGCGGCTTTTACGGGTGGA 1330
QY 1344 TTTGTAGCGTGGGCTCCACATGAGATTTCTGGTGTGCGCGGCTTGGCCAGAAAGGCTGCA 1403
Db 1331 TTTGTAGCGTGGGCTCCACATGAGATTTCTGGTGTGCGCGGCTTGGCCAGAAAGGCTGCA 1390
QY 1404 AGATGTCGAGTCTCTGGGTGGCTCCAGACTGAGTTCCTTAGCTTCCAGATGGGGATTT 1463
Db 1391 AGATGTCGAGTCTCTGGGTGGCTCCAGACTGAGTTCCTTAGCTTCCAGATGGGGATTT 1449
QY 1464 CCCTACCAAGATTTGTGACACAGATATATCCAGTACCCAACTACTGTCTCTCAAAAG 1523
Db 1450 CCCTACCAAGATTTGTGACACAGATATATCCAGTACCCAACTACTGTCTCTCAAAAG 1509
QY 1524 CCAGCAGTGTCTGATGAGAAACCGCAATCGGAGGTGTCGCCATGAGATGTCTGCAGAA 1583
Db 1510 CCAGCAGTGTCTGATGAGAAACCGCAATCGGAGGTGTCGCCATGAGATGTCTGCAGAA 1569
QY 1584 TGAGACTTACAGTGCCTGAGCCCTGGCAAAAGTGAGGAGTGTGTGCTTCGATGAGGCA 1643
Db 1570 TGAGACTTACAGTGCCTGAGCCCTGGCAAAAGTGAGGAGTGTGTGCTTCGATGAGGCA 1629
QY 1644 GAGTTCAGCACCTTCACTTAGGCGAGTTCGATGAGTGCCTGTATTTTCGCCACAC 1703
Db 1630 GAGTTCAGCACCTTCACTTAGGCGAGTTCGATGAGTGCCTGTATTTTCGCCACAC 1689
QY 1704 CCAGCCCCAACCCTGCCACCTTCTCTATTTGTTTTCAGACCCCATGCTTTCAGGCTGCC 1763
Db 1690 CCAGCCCCAACCCTGCCACCTTCTCTATTTGTTTTCAGACCCCATGCTTTCAGGCTGCC 1749
QY 1764 CTTCTGGGCTGTGTTACTCGGCCCTTACTCAGATTTCTTGGTGGAGCAACAGTCCAG 1823
Db 1750 CTTCTGGGCTGTGTTACTCGGCCCTTACTCAGATTTCTTGGTGGAGCAACAGTCCAG 1809
QY 1824 AGAGGCCACGTTGGAGCTGCGCCCTCTCTTAAAGATGACTTTTACATAAATGTTGATC 1883
Db 1810 AGAGGCCACGTTGGAGCTGCGCCCTCTCTTAAAGATGACTTTTACATAAATGTTGATC 1868

QY 1884 TTCAAAAAAAA 1895
Db 1869 TTCAAAAAAAA 1880

RESULT 7

US-10-653-595-90
; Sequence 90, Application US/10653595
; Publication No. US20040048304A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1C1
; CURRENT APPLICATION NUMBER: US/10/653,595
; CURRENT FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: US 09/397945
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 1892
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-653-595-90

Query Match 95.6%; Score 1811.2; DB 17; Length 1892;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1860; Conservative 0; Mismatches 8; Indels 4; Gaps 4;
QY 24 GGACGGGGCGGATCTTCTCGGCCATGAGGAGCCGCGCTGGCTTCTTCCCTCACT 83
Db 13 GGGACCGGACGGATCTTCTCGGCCATGAGGAGCCGCGCTGGCTTCTTCCCTCACT 72
QY 84 CTTGAAGTGTGCTGCTCTGCTCTGCGCATGCGACCTCGCAGCCAGGATTCGACTCAGGCC 143
Db 73 CTTGAAGTGTGCTGCTCTGCTCTGCGCATGCGACCTCGCAGCCAGGATTCGACTCAGGCC 132
QY 144 CACTCCAGCAGCCCTCTCTCTCTACCGAATACGAACTGCTTTCGCACTGCTGACTCC 203
Db 133 CACTCCAGCAGCCCTCTCTCTCTACCGAATACGAACTGCTTTCGCACTGCTGACTCC 192
QY 204 AACCTGGAAGGAGAGACTTACCTGCGTCCGCAACCCACCGCTCCCGGAATCCCA 263
Db 193 AACCTGGAAGGAGAGACTTACCTGCGTCCGCAACCCACCGCTCCCGGAATCCCA 252
QY 264 ACTCGTCCAGCTGGACCAATATGAAACACCGCTTAGTCCCGATGCTGCTGCTC 323
Db 253 ACTCGTCCAGCTGGACCAATATGAAACACCGCTTAGTCCCGATGCTGCTGCTC 312
QY 324 CAACTCCCTTATGCTCTGCTTGTAGTCTTTCTGCGAGTTCACCTCACTACCGTTC 383
Db 313 CAACTCCCTTATGCTCTGCTTGTAGTCTTTCTGCGAGTTCACCTCACTACCGTTC 372


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QY 384 CAACCACTCTACTATGCGCAAGAGAGTCTGTGTTCCTCCAGCCAGTCTCTATTCTCTCACC 443
Db 373 CAACCACTCTACTATGCGCAAGAGAGTCTGTGTTCCTCCAGCCAGTCTCTATTCTCTCACC 432
QY 444 TAACTCTCAAGAGATAGAAAGCTTCAGTGAAGTCTCAACCAACAGATGACCTCCCC 503
Db 433 TAACTCTCAAGAGATAGAAAGCTTCAGTGAAGTCTCAACCAACAGATGACCTCCCC 492
QY 504 CATCTCACCCCACTTCAAGTACAGACGCGCAGACCTTCCAGCCCTGCGCTGAGAGGCT 563
Db 493 CATCTCACCCCACTTCAAGTACAGACGCGCAGACCTTCCAGCCCTGCGCTGAGAGGCT 552
QY 564 CAGCAACAACGTGGAGAGCTCTCAATCTCTCTTGTCTCCCTGGAGGCGCAGGAGCAAGC 623
Db 553 CAGCAACAACGTGGAGAGCTCTCAATCTCTCTTGTCTCCCTGGAGGCGCAGGAGCAAGC 612
QY 624 GCAGAGCAACAGCAGGAGCAAGAGTGGAGCAAGGAGGAGTGTCTCAGCTGCAGACAGCTC 683
Db 613 GCAGAGCAACAGCAGGAGCAAGAGTGGAGCAAGGAGGAGTGTCTCAGCTGCAGACAGCTC 672
QY 684 GCAGGAGGAGGAGCAAGAGCAAGAGCAAGAGGAGCAAGAGGAGGAGGAGCAAGCA 743
Db 673 GCAGGAGGAGGAGCAAGAGCAAGAGCAAGAGGAGCAAGAGGAGGAGGAGCAAGCA 732
QY 744 GGAAGAAGGACAGGAGCAAGAGGAGCAAGAGGAGTGTCTCAGCTGCAGACAGCTC 803
Db 733 GGAAGAAGGACAGGAGCAAGAGGAGCAAGAGGAGTGTCTCAGCTGCAGACAGCTC 792
QY 804 AGAGCCCAAGTTTCACTCTGAATCTCTATCTTCTTAAACCTTCTCTTTTGTCTCCCGGT 863
Db 793 AGAGCCCAAGTTTCACTCTGAATCTCTATCTTCTTAAACCTTCTCTTTTGTCTCCCGGT 852
QY 864 ACAGAGAGTAGAGTCTACTCTCTATGATATGAGAACATCCAGGAGCTCATTCGATCAGC 923
Db 853 ACAGAGAGTAGAGTCTACTCTCTATGATATGAGAACATCCAGGAGCTCATTCGATCAGC 912
QY 924 CCAGGAAATAGATGAATGAATGAATATATGATGAGAACTCTACTGGAGAAACCAAAA 983
Db 913 CCAGGAAATAGATGAATGAATGAATATATGATGAGAACTCTACTGGAGAAACCAAAA 972
QY 984 CCTGCGAGCTCTCTGAGCTGCCCCACACAGAGGCTTGTGTGTGTCTGTCTATTCGAT 1043
Db 973 CCTGCGAGCTCTCTGAGCTGCCCCACACAGAGGCTTGTGTGTGTCTGTCTATTCGAT 1031
QY 1044 CGTGGAGATACCTGATATATACCCCAAGCAGGCAAGGCTGGAAGTATGAGAGGAGCA 1103
Db 1032 CGTGGAGATACCTGATATATACCCCAAGCAGGCAAGGCTGGAAGTATGAGAGGAGCA 1091
QY 1104 GATCTTGTGTTCGGGAAGTCTGTGACAGCTTGGCGGCGACATGTCTACCTG 1163
Db 1092 GATCTTGTGTTCGGGAAGTCTGTGACAGCTTGGCGGCGACATGTCTACCTG 1151
QY 1164 TGCCCTCTGTGACTTCTGCTCTCTGAGCTGGAGCAGTGCCACTCAGAGGCGAGCTGCA 1223
Db 1152 TGCCCTCTGTGACTTCTGCTCTCTGAGCTGGAGCAGTGCCACTCAGAGGCGAGCTGCA 1211
QY 1224 GCGGCAACATGCGACACCTCCCAAGACTCTCTTGTGAGCCCTTGTCTGCTCCCA 1283
Db 1212 GCGGCAACATGCGACACCTCCCAAGACTCTCTTGTGAGCCCTTGTCTGCTCCCA 1270
QY 1284 GAGCTGTCCATCGGCAACAGGTAGGTCCTCCAGATCAGGCGCTTTTACGGGCTGGA 1343
Db 1271 GAGCTGTCCATCGGCAACAGGTAGGTCCTCCAGATCAGGCGCTTTTACGGGCTGGA 1330
QY 1344 TTTGTACGGTGGGCTCCACATGAGCTTCTGGTGTGCGCGGCTTGCACAGAAAGGCTGCA 1403
Db 1331 TTTGTACGGTGGGCTCCACATGAGCTTCTGGTGTGCGCGGCTTGCACAGAAAGGCTGCA 1390
QY 1404 AGATGTCGAGTCTCTGGGTGGCTCCAGACTGAGTCTTCTAGCTTCCAGATGGGATTT 1463
Db 1391 AGATGTCGAGTCTCTGGGTGGCTCCAGACTGAGTCTTCTAGCTTCCAGATGGGATTT 1449
QY 1464 CCTACCAAGATTTGTGACACAGACTATATCCAGTACCCAAACTACTGTCTCTCAAAAG 1523
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Db 1450 CCTACCAAGATTTGTGACACAGACTATATCAGTACCCAAACTACTGTCTCTCAAAAG 1509
QY 1524 CCAGCAGTGTCTGATGAGAAACCGCAATCGGAAGGTGTCCCGCATGAGATGTCTGCAGAA 1583
Db 1510 CCAGCAGTGTCTGATGAGAAACCGCAATCGGAAGGTGTCCCGCATGAGATGTCTGCAGAA 1569
QY 1584 TGAGACTTACAGTGTGCGCTGAGCCCTGGCAAAAGTGGAGAGCTTGTCTCGATGGAGCCA 1643
Db 1570 TGAGACTTACAGTGTGCGCTGAGCCCTGGCAAAAGTGGAGAGCTTGTCTCGATGGAGCCA 1629
QY 1644 GGAGTTTCAGCAGCTTTCAGCTCTAGGCGCAGTTCGGATGAGCTGGCGTCTATTCTCCCAAC 1703
Db 1630 GGAGTTTCAGCAGCTTTCAGCTCTAGGCGCAGTTCGGATGAGCTGGCGTCTATTCTCCCAAC 1689
QY 1704 CCAGCCCAACCTGCGCAGCTTCTATTGTTTGTGAGACCCCATTTGCTTTTCAGGCTGCC 1763
Db 1690 CCAGCCCAACCTGCGCAGCTTCTATTGTTTGTGAGACCCCATTTGCTTTTCAGGCTGCC 1749
QY 1764 CTTCTGGGTCTCTTACTCGGCCCTTACTCACAATTTCTTGGGTGGAGCAACAGTCCCAG 1823
Db 1750 CTTCTGGGTCTCTTACTCGGCCCTTACTCACAATTTCTTGGGTGGAGCAACAGTCCCAG 1809
QY 1824 AGAGGCCACAGCTGGGAGCTGGGCCCTCTCTTAAAGATGACTTTACATAAATGTTGATC 1883
Db 1810 AGAGGCCACAGCTGGGAG-TGGGCCCTCTTAAAGATGACTTTACATAAATGTTGATC 1868
QY 1884 TTTCAAAAAAAA 1895
Db 1869 TTTCAAAAAAAA 1880

RESULT 8
US-10-085-117-54
; Sequence 54, Application US/10085117
; Publication No. US2003023334A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 1632
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-117-54

Query Match 86.1%; Score 1632; DB 17; Length 1632;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1632; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 ATGAGAAAGCCAGCGCTGCTTCTTCCCTCACTCTCTGAAAGTGTCTCTGCTCTG 108
Db 1 ATGAGAAAGCCAGCGCTGCTTCTTCCCTCACTCTCTGAAAGTGTCTCTGCTCTG 60
QY 109 GCACCTGCGGAGCCAGGATTCGACTCAGGCCCCCACTCCAGGCGCCCTCTCTCTCT 168
Db 61 GCACCTGCGGAGCCAGGATTCGACTCAGGCCCCCACTCCAGGCGCCCTCTCTCTCT 120
QY 169 ACCGAATACGAACGCTTCTTGGCACTGTCTCACTCTCACTCTGAAAGTGTCTCTCTCT 228
Db 121 ACCGAATACGAACGCTTCTTGGCACTGTCTCACTCTCACTCTGAAAGTGTCTCTCTCT 180
QY 229 CGTCTCCGTGCAACCCAGGCTGCGGAAATCCACACTCGTCCAGTGGACCAATATGAA 288
Db 181 CGTCTCCGTGCAACCCAGGCTGCGGAAATCCACACTCGTCCAGTGGACCAATATGAA 240
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QY 289 AACACAGGCTTAGTGGCCGATGGTGTCTGTCTGCTTCAACCTCCCTTATGCTCTCTGGTTT 348
Db |||||
QY 241 AACACAGGCTTAGTGGCCGATGGTGTCTGTCTGCTCAACCTCCCTTATGCTCTCTGGTTT 300
Db |||||
QY 349 GAGTCTTTCTGCGAGTTCACTACTACCGTGTCTCAACCAAGCTTACTATGCGCAAGAGA 408
Db |||||
QY 301 GAGTCTTTCTGCGAGTTCACTACTACCGTGTCTCAACCAAGCTTACTATGCGCAAGAGA 360
QY 409 GTCTGTGTTTCCAGCCAGTCTCTATCTCTCTCACTAACTCTCAAGGAGATAGAAGCT 468
Db |||||
QY 361 GTCTGTGTTTCCAGCCAGTCTCTATCTCTCACTAACTCTCAAGGAGATAGAAGCT 420
Db |||||
QY 469 TCAGCTGAAGTCTCAACCAAGTGTCTCTCTCACTAACTCTCAAGGAGATAGAAGCT 420
Db |||||
QY 421 TCAGCTGAAGTCTCAACCAAGTGTCTCTCTCACTAACTCTCAAGGAGATAGAAGCT 420
Db |||||
QY 529 GAACGCCAGCTTCCAGCCCTGCGCTGAGAGGCTCAAGCAACCTGGAAGAGCTCTCTA 588
Db |||||
QY 481 GAACGCCAGCTTCCAGCCCTGCGCTGAGAGGCTCAAGCAACCTGGAAGAGCTCTCTA 540
Db |||||
QY 589 CAATCTCTCTTGTCTTGGAGGCCAGGAGCAAGCCGAGAGCACAGCAGGAGCAAGGA 648
Db |||||
QY 541 CAATCTCTCTTGTCTTGGAGGCCAGGAGCAAGCCGAGAGCACAGCAGGAGCAAGGA 600
QY 649 GTGAGCACAGGAGGAGCCGACACAGAGACACAGCAGGAGAGAGGCGAGAGCAAGGA 708
Db |||||
QY 601 GTGAGCACAGGAGGAGCCGACACAGAGACACAGCAGGAGAGAGGCGAGAGCAAGGA 660
QY 709 GAGCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 768
Db |||||
QY 661 GAGCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 769 GGACGGAGGCTGTGTCTCAGCTGACAGCAGACTCAGAGCCCAAGTTTCACTCTGAATCT 828
Db |||||
QY 721 GGACGGAGGCTGTGTCTCAGCTGACAGCAGACTCAGAGCCCAAGTTTCACTCTGAATCT 828
QY 829 CTATCTTTCAACCTTCTTTTGTCTCCCGGGTACGAGAGGAGTCTACTCTCTATG 888
Db |||||
QY 781 CTATCTTTCAACCTTCTTTTGTCTCCCGGGTACGAGAGGAGTCTACTCTCTATG 840
QY 889 ATATGGAGAACATCCAGGAGCTCATTCGATCAGCCAGGAGGAGGAGGAGGAGGAGGAG 948
Db |||||
QY 841 ATATGGAGAACATCCAGGAGCTCATTCGATCAGCCAGGAGGAGGAGGAGGAGGAGGAG 900
QY 949 ATATATGATGAGAACTCTCTACTGAGAGAACCAAACTCTGCGAGCTTCTGCGAGTGCC 1008
Db |||||
QY 901 ATATATGATGAGAACTCTCTACTGAGAGAACCAAACTCTGCGAGCTTCTGCGAGTGCC 960
QY 1009 CACACAGAGGCTTGT 1068
Db |||||
QY 961 CACACAGAGGCTTGT 1020
QY 1069 CCCACAGCAAGGCTTGGAGTACATGAGAGGAGATCTTTGGTTTGGGAGGTCGCTC 1128
Db |||||
QY 1021 CCCACAGCAAGGCTTGGAGTACATGAGAGGAGATCTTTGGTTTGGGAGGTCGCTC 1080
QY 1129 TGTGAGAGCTTGGGCGGACACATGTCTACTGTGCGCTCTGTGACTTCTGTCTCTG 1188
Db |||||
QY 1081 TGTGAGAGCTTGGGCGGACACATGTCTACTGTGCGCTCTGTGACTTCTGTCTCTG 1140
QY 1189 AAGCTGAGAGCTGACCTCAGAGGCGGAGCTGAGCGGCAACATGCGACCTCCAC 1248
Db |||||
QY 1141 AAGCTGAGAGCTGACCTCAGAGGCGGAGCTGAGCGGCAACATGCGACCTCCAC 1200
QY 1249 AAGCTTCTTGTGAGCCCTTGTGCTTCCAGAGGCTGTCATCGGCAACAGGTA 1308
Db |||||
QY 1201 AAGCTTCTTGTGAGCCCTTGTGCTTCCAGAGGCTGTCATCGGCAACAGGTA 1260
QY 1309 GGGTCCCAGATCAGGCGGCTTTTACGGGCTGATTTGACGGTGGCTTCCATGAGAC 1368
Db |||||
QY 1261 GGGTCCCAGATCAGGCGGCTTTTACGGGCTGATTTGACGGTGGCTTCCATGAGAC 1320
QY 1369 TTCTGTGTGCGGCTTGGCAAGAAAGGCTGTGAAGATGTCCGAGTCTCTGGTGGCTC 1428

Db |||||
QY 1321 TTCTGTGTGCGCGCTTGCACGAAGGCTGTGAAGATGTCCGAGTCTCTGGTGGCTC 1380
QY 1429 CAGACTGAGTCTCTTACCTTCCAGGATGGGATTTCCCTTACCAGATTTGTGACACAGAC 1488
Db |||||
QY 1381 CAGACTGAGTCTCTTACCTTCCAGGATGGGATTTCCCTTACCAGATTTGTGACACAGAC 1440
QY 1489 TATATCCAGTACCACCAACTACTGTTCCTTCAAAAGCCAGCAGTGTCTGATGAGAAACCGC 1548
Db |||||
QY 1441 TATATCCAGTACCACCAACTACTGTTCCTTCAAAAGCCAGCAGTGTCTGATGAGAAACCGC 1500
QY 1549 AATCGGAAGGTGTCCGCATGAGATGTCTGCAAGATGAGCTTACAGTGGCTGAGCCCT 1608
Db |||||
QY 1501 AATCGGAAGGTGTCCGCATGAGATGTCTGCAAGATGAGCTTACAGTGGCTGAGCCCT 1560
QY 1609 GGCAGAAAGTGAAGCAGTGTTCCTTCCGATGAGCAGGAGTTCAGCCTTGAAGCTTAGGC 1668
Db |||||
QY 1561 GGCAGAAAGTGAAGCAGTGTTCCTTCCGATGAGCAGGAGTTCAGCCTTGAAGCTTAGGC 1620
QY 1669 CAGTTCCGATGA 1680
Db |||||
QY 1621 CAGTTCCGATGA 1632

RESULT 9

US-10-296-115-693
; Sequence 693, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 693
; LENGTH: 1671
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-115-693

Query Match
Best Local Similarity 67.1%; Score 1271.8; DB 17; Length 1671;
Matches 1273; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 91 GTGTGTCTCTGCTCTGCGACCTGCGCAGCCAGGATTCGACTCAGCCCTCCACTCCA 150
Db |||||
QY 397 GTGTGTCTCTGCTCTGCGACCTGCGCAGCCAGGATTCGACTCAGCCCTCCACTCCA 456
Db |||||
QY 151 GGCAGCCCTCTCTCTCTACCGAATACGAAACGCTTCTGCGACTGCTGACTCCACCTGG 210
Db |||||
QY 457 GGCAGCCCTCTCTCTCTACCGAATACGAAACGCTTCTGCGACTGCTGACTCCACCTGG 516
QY 211 AAGCAGAGACTACCTGCGCTCTGCGCAACCCAGCGCTGCGGAATCCACACTCGTC 270
Db |||||
QY 517 AAGCAGAGACTACCTGCGCTCTGCGCAACCCAGCGCTGCGGAATCCACACTCGTC 576
QY 271 CAGCTGCAATATGAAACCAACCGCTTAGTGGCCGATGGTGTCTGCTCCAACTC 330
Db |||||
QY 577 CAGCTGCAATATGAAACCAACCGCTTAGTGGCCGATGGTGTCTGCTCCAACTC 636
QY 331 CTTATGCTCTCTGTTGAGTCTTCTGCGAGTCTCACTACCTGCTGCTCCAACTC 390
Db |||||
QY 637 CTTATGCTCTCTGTTGAGTCTTCTGCGAGTCTCACTACCTGCTGCTCCAACTC 696
QY 391 GTCTACTATGCAAGAGAGTCTGTTCCAGCGAGTCTTCTTCTTCTTCTTCTTCTTCTTCT 450
Db |||||
QY 697 GTCTACTATGCAAGAGAGTCTGTTCCAGCGAGTCTTCTTCTTCTTCTTCTTCTTCTTCT 756

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QY 451 CTCAGGAGATAGAGCTTCAGCTGAAGTCTCACCCACACGATGACCTCCCCCATCTCA 510
Db 757 CTCAGGAGATAGAGCTTCAGCTGAAGTCTCACCCACACGATGACCTCCCCCATCTCA 816
QY 511 CCCCACTTCACAGTGCAGAGCCAGACCTTCCAGCCCTGCGCTGAGAGGCTCAGCAAC 570
Db 817 CCCCACTTCACAGTGCAGAGCCAGACCTTCCAGCCCTGCGCTGAGAGGCTCAGCAAC 876
QY 571 AACGTGGAAGACTCTCAATCTCTTGTCTCCCTGGAGGCGCAGAGCAAGGCCAGAG 630
Db 877 AACGTGGAAGACTCTCAATCTCTTGTCTCCCTGGAGGCGCAGAGCAAGGCCAGAG 936
QY 631 CACAAGCAGGAGCAAGAGCTGGAGCACAGGCGAGGCGCACCAAGAACACAAAGCAGGAA 690
Db 937 CACAAGCAGGAGCAAGAGCTGGAGCACAGGCGAGGCGCACCAAGAACACAAAGCAGGAA 996
QY 691 GAGGGGCGAANAACAGGAAGAGCAAGAGGAAACAGGAAGAGGAGGAGGAGGAGGAGAA 750
Db 997 GAGGGGCGAANAACAGGAAGAGCAAGAGGAAACAGGAAGAGGAGGAGGAGGAGGAGAA 1056
QY 751 GGACAGGGGACTAAGGAGGAGCGGAGGCTGTCTCAGCTCGACAGACACTCAGAGCCC 810
Db 1057 GGACAGGGGACTAAGGAGGAGCGGAGGCTGTCTCAGCTCGACAGACACTCAGAGCCC 1116
QY 811 AAGTTTCACTCTGAATCTCTATCTTCTAACCCTTCTCTTTTGTCTCCCGGCTACGAGAA 870
Db 1117 AAGTTTCACTCTGAATCTCTATCTTCTAACCCTTCTCTTTTGTCTCCCGGCTACGAGAA 1176
QY 871 GTAGAGTCTACTCTTATGATATATGAGAAACATCCAGGAGCTCATTCGATCAGCCCGAGAA 930
Db 1177 GTAGAGTCTACTCTTATGATATATGAGAAACATCCAGGAGCTCATTCGATCAGCCCGAGAA 1236
QY 931 ATAGATGAATCAATGAATATATGATGAGAACTCTTACTTGAGAAACCAAAACCCCTGGC 990
Db 1237 ATAGATGAATCAATGAATATATGATGAGAACTCTTACTTGAGAAACCAAAACCCCTGGC 1296
QY 991 AGCTTCTCTGACGTGCCCCACACAGAGGCTTGTGTGTCTGTCTATTCGATCGTGGAG 1050
Db 1297 AGCTTCTCTGACGTGCCCCACACAGAGGCTTGTGTGTCTGTCTATTCGATCGTGGAG 1356
QY 1051 AATACCTGCATCATAAACCCCAACAGCCAGGCTTGAAGTACATGAGGAGGAGATCCTT 1110
Db 1357 AATACCTGCATCATAAACCCCAACAGCCAGGCTTGAAGTACATGAGGAGGAGATCCTT 1416
QY 1111 GGTTCGGGAAGTGGTCTGTGACAGCTTGGGCGGCGACATGTCTACTGTGCGCTC 1170
Db 1417 GGTTCGGGAAGTGGTCTGTGACAGCTTGGGCGGCGACATGTCTACTGTGCGCTC 1476
QY 1171 TGTGACTTCTGCTTCTTGAAGCTGGAGCAGTGCCACTCAGAGGCCAGCTCGAGCGGCAA 1230
Db 1477 TGTGACTTCTGCTTCTTGAAGCTGGAGCAGTGCCACTCAGAGGCCAGCTCGAGCGGCAA 1536
QY 1231 CAATCGCACACCTCCCAAGACTCCCTTGTGAGCCCTTGTGAGCCCTCCAGAGCCTG 1290
Db 1537 CAATCGCACACCTCCCAAGACTCCCTTGTGAGCCCTTGTGAGCCCTCCAGAGCCTG 1596
QY 1291 TCCATCGGCAACAGGAGGCTTCCAGAAATCAGCGCGCTTTTACGGGCTGATTGTAC 1350
Db 1597 TCCATCGGCAACAGGAGGCTTCCAGAAATCAGCGCGCTTTTACGGGCTGATTGTAC 1656
QY 1351 GGTGGGCTCCACATG 1365
Db 1657 GGTGGGCTCCACATG 1671
```

RESULT 10

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US-10-085-117-50
; Sequence 50, Application US/10085117
; Publication No. US2003023334A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
```

```
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 1840
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-085-117-50
```

Query Match 59.5%; Score 1128.2; DB 17; Length 1840;

Best Local Similarity 77.5%; Pred. No. 0; Mismatches 398; Indels 15; Gaps 4;

Matches 1422; Conservative 0;

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QY 26 AGCCGGGGGATCTTCTCCGGCCATGAGGAAGCCAGCCGCTGCTTCTTCCCTCACTCC 85
Db 13 AGCCGGGGTGGATCTTCCAGGCCATGATGATCTAGCTGCTGCTTCTTCTGATGCTTC 72
QY 86 TGAAGGTGCTGCTCTGCTCTGCTCTGCGCACCTGCGCGAGCCAGGATTCGACTCAGGCCCCCA 145
Db 73 TGAAGGTGCTGCTCTGCTCTGCGCACCTGCGCGAGGATTCGCGCTGAGGAAT--CTCCAGCCTCCA 129
QY 146 CTCAGGCGAGCCCTCTCTCTCTACCGAATACGAACGCTTCTTGGCACTGCTGACTCCA 205
Db 130 CTCAGGCGAGCCCTCTCTCTCTACCGAATACGAACGCTTCTTGGCGCTGCTGACTCCA 189
QY 206 CTTGAAGCGAGAGACTACTCTGCTCTGCGCACCTGCGCGAACCCAGCGCTCCCGGAATCCCAAC 265
Db 190 CTTGAAGCGAGAGACTACTCTGCTCTGCGCACCTGCGCGAACCCAGCGCTCCCGGAATCCCAAC 249
QY 266 TCGTCCAGCTGACCAATATGAAAAACACGGCTTAGTGTCCGATGCTGTCTGTCTCCA 325
Db 250 TCGTTCAGTTCGATCAATATGAAAAACACGGATTCGTACCGATGCTGTCTGTCTCCG 309
QY 326 ACCTCCCTTATGCTCTCTGCTTGTGAGTCTTCTGCGAGTTCATCTACTACCTGCTGCTCCA 395
Db 310 ATCTCCCTTATGCTCTCTGCTTGTGAGTCTTCTGCGAGTTCGTCTAGTATCGTGTCTCCA 369
QY 386 ACCAGCTCTACTATGCCAAGAGAGTCTGCTGTGTTTCCAGCGAGTCTCTTCTCTACCTTA 445
Db 370 ACCATGCTCTATATGCCAAGAGGCTGCTGCTGCTCCAGCGCTCTCCATCTCTATCCCCA 429
QY 446 ACCTCTCAAGGAGATAGAAGCTTCAGCTGAAGTCTACCCCAACACGATGACCTTCCCCCA 505
Db 430 ACCTCTCAAGGAGTGGAGTCTTCAGCAGAGAGTTCCTCCCACTTCCATGACCAACCCCA 489
QY 506 TCTCAACCCACTTCACTGAGACAGAACCGCAGACCTTCAGCGCTTGGCTGAGAGCTCA 565
Db 490 TTGTGTCCCATGCCCCACAGCCACAGAACACAGGCTTCCAGCGCTTGGCTGAGCGCTCA 549
QY 566 GCACAACAGTGGAGAGCTCTTACAACTCTCTTGTCTGCTGCGAGGCGCAGGAGCAAGCGC 625
Db 550 ACAACAACAGTGGAGAGTCTGCTGAGTCTATCTTGTCTGCGAGGAGGAGGAGCAACAGA 609
QY 626 CAGAGCAACAAGCAGGAGCAAGAGTGGAGCAGCAGGAGGAGCGGACACAGAAGAACACAAGC 685
Db 610 GCAGTCGAGAGCAGGCCA---GGAGCAGACACAGCAGGAGCAGATCCAGAACATNAGC 666
QY 686 AGGAAGGGGCGAAGAACAGGAAGAGC---AAGAAGAGGAACAGGAAGAGGAGGAGGAGC 742
Db 667 TAGAAGAGCGCAGGAGCAAGAGCAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGC 726
QY 743 AGGAAGAGGAGCAGGGGACTAAGGAGGAGCGGAGGCTGTCTCTCAGCTGCGACAGACT 802
Db 727 AGGAAGGGGCGAGGGGACAGAGCGGGTCTGAGTCTAGTGTCCAGGCTGCGAGTCA 786
QY 803 CAGAGCCCAAGTTTCACTCTGAATCTCTATCTTCTTAACCTTCTCTTCTTCTTCTTCTTCT 862
Db 787 CAGAGCCCAAGTTTCAATCCCAAGTCACTGTCTTCCAAACCCGCTCTTCTTCTTCTTCTTCT 846
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[illegible]

```

; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-085-117-51

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Query Match	56.1%	Score 1062.6	DB 17	Length 1623
Best Local Similarity	79.9%	Pred. No. 6.3e-312		
Matches 1306	Conservative 0	Mismatches 314	Indels 15	Gaps 4
QY	49	ATGAGGAGCCAGCGGCTGGCTTCCCTCACTCCTGAAGGTGCTGCTCGTCTCTG 108		
Db	1	ATGATGAATAGTGTGTGCTTCTTCTGTATGCTTCTGGAAGTGTCTCTCGCTCGA 60		
QY	109	GCACCTCGCGCAGCCAGGATTCGACTCAGGCCCCCACTCCAGGCAGGCCCTCTCTCCT 168		
Db	61	ACACTCTTTCCGCTGAGGAAT---CTCAGAGCTTCCTCCAGGAGGCCCTCTCTCGTCC 117		
QY	169	ACCGAATACGAACGCTTCTTCGCACTGTGACTCCAACTCGAAGGCAGAGACTACCTGC 228		
Db	118	ACTGAGTATGAACGCTTCTTCGCCCTGTGTGACCCCAACTCGGAAGGCAGACCACTGC 177		
QY	229	CGTCTCCGTGCAACCCAGCGCTGCGGAATCCCACTGTCTCAGCTTGACCAATATGAA 288		
Db	178	CGCTTCGTGCACCCACCGCTGCGGGAACCCCACTCTCTGTTCAAGTTGGATCAATATGAA 237		
QY	289	AACCA CGGCTTAGTGCCGATGGTGTGTCTGTCTCCAACTCCCTATGCTCTCTCGTTT 348		
Db	238	AACCACGGAATGGTACAGATGGTGTGTGTCTGCTCCGATCTCCCTTATGCTTCTCGTTT 297		
QY	349	GAGTCTTTCTGCCAGTTCACTCACTACGTTGTCTCCAAACAGCTACTATGCCAAGAGA 408		
Db	298	GAGTCTTTCTGCCAGTTTCTCAGTATCGTTGTCTCCAACTATGTCTACTATGCCAAGAG 357		
QY	409	GTCTGTGTTCCCGACGACTCTTATTTCTCACTAACACTCTCAAGGAGATAGAGCT 468		
Db	358	GTCCGGTGTCTCCAGCCGCTCTCCATCTATCTCCCAACACTCTCAAGGAGTGGAGTCT 417		
QY	469	TCAGCTGAAGTCTCACCAACACGATGACTTCCCCATCTCACCCCACTTCAAGTGA 528		
Db	418	TCAGCAGAAGTTCTCTCCCACTTCCATGACCAACCCCACTTGTGCCATGCCACAGCCACA 477		
QY	529	GAACGCCAGACCTTCCAGCCTTGCGCTGAGAGGCTCAGCAACACTGGAAGAGTCTCTA 588		
Db	478	GAACACAGGCTTTCAGGCTTGGCTTGAGGGCTCAACAACAACTGAGGAGTGTGTG 537		
QY	589	CAATCTCTTGTCTCGGAGGCCAGGAGCAAGCGCCAGAGCAACGAGGAGCAAGGAGCAAG 648		
Db	538	CAGTCATCTTGTCTCGGAGGCCAGGAGCAAGCAACAGAGCAGTCCGAGACACAGGCCA---G 594		
QY	649	GTGGAGCAAGCGAGGCCACACAGAACACAGCAGGAGAGGGGAGAGAAACAGGAA 708		
Db	595	GAGCAGCAACAGCAGGAGCAGTCCAGAACATTAAGCTAGAAGAGCGCAGGAGCAAGAA 654		
QY	709	GAGC---AAGAAGAGGAACAGGAAGAGGGGAGGAAAGCAGGAAGAGGACAGGGGACTAAG 765		
Db	655	GAGCAGGAAGAAGAGGAAGAGGAGGAGAGCCACACGAGGAAGAGGGCAGGGGACAGAG 714		
QY	766	GAGGACCGGGAGGCTGTGTCTCAGCTGCAGACAGACTCAGAGCCCAAGTTTCACTCTGAA 825		
Db	715	GCGGTCTGGAGTCAGTGTCCAGGCTGCACTCAGACTCAGAGCCCAAGTTTCAATCCCAAG 774		

QY 762 TAAGGAGGACGGAGCGTGTCTCAGCTGCAGACAGACTCAGAGCCCAAGTTTCACATC 821
DB 13052 TAAGGAGGACGGAGCGTGTCTCAGCTGCAGACAGACTCAGAGCCCAAGTTTCACATC 13111
QY 822 TGAATCTCTATCTTCTAACCCTTCTCTTTTGTCTCCCGGGTACGAGAAAGTAGAGTCTAC 881
DB 13112 TGAATCTCTATCTTCTAACCCTTCTCTTTTGTCTCCCGGGTACGAGAAAGTAGAGTCTAC 13171
QY 882 TCCTATGATAATGGAGAAATCCAGAGCTCATTTCGATCAGCCCGGAAATAGATCAAT 941
DB 13172 TCCTATGATAATGGAGAAATCCAGAGCTCATTTCGATCAGCCCGGAAATAGATCAAT 13231
QY 942 GAATGAAATATATGATGAGAACTCTTACTGGAGAAACCAAACTTGGAGAAATAGATCAAT 1001
DB 13232 GAATGAAATATATGATGAGAACTCTTACTGGAGAAACCAAACTTGGAGAAATAGATCAAT 13291
QY 1002 GCT 1004
DB 13292 GTT 13294

RESULT 15

US-09-918-995-14842
; Sequence 14842, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14842
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(469)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-14842

Query Match 22.9%; Score 433.8; DB 10; Length 469;
Best Local Similarity 96.1%; Pred. No. 6e-121;
Matches 441; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 907 GAGCTCATTCGATCAGCCCGAGGAAATAGATGAAATGAAATATATGATCAGAACTCC 966
DB 11 GAGTCCNTAGCNCAGNGGNGGAANTCTGAAATGAAATGAAATATATGATCAGAACTCC 70
QY 967 TACTGGAGAAACCAACCTGGAGCTTCTGTCAGCTGCCCGACACAGAGGCTTGTG 1026
DB 71 TACTGGAGAAACCAACCTGGAGCTTCTGTCAGCTGCCCGACACAGAGGCTTGTG 130
QY 1027 GTGCTGTGCTATTTCGATCGTGAGAAATACCTCATCAACCCCAAGCCCTGG 1086
DB 131 GTGCTGTGCTATTTCGATCGTGAGAAATACCTCATCAACCCCAAGCCCTGG 190
QY 1087 AAGTACATGGAGAGAGATCCTTGGTTTCGGAAAGTCGGTCTGTGACAGCCTTGGGGG 1146
DB 191 AAGTACATGGAGAGAGATCCTTGGTTTCGGAAAGTCGGTCTGTGACAGCCTTGGGGG 250
QY 1147 CGACATGCTTACCTGTGCTCTGTGCTTCTGTGCTTCTGTGCTGAGCTGAGAGAGTCCAC 1206
DB 251 CGACATGCTTACCTGTGCTCTGTGCTTCTGTGCTTCTGTGCTTCTGTGCTGAGCTGCCAC 310
QY 1207 TCAGAGGCGAGCTTCAGCGGCAAAATGCGACACCTCCCAAGACTCCCTTTGTGAGC 1266

DB 311 TCAGAGGCGAGCTTCAGCGGCAAAATGCGACACCTCCCAAGACTCCCTTTGTGAGC 370
QY 1267 CCCTTGTCTTCCCTCCAGAGCTTCCATCGGCAACAGGTAGGGTCCCGAGAAATCAGGC 1326
DB 371 CCCTTGTCTTCCCTCCAGAGCTTCCATCGGCAACAGGTAGGGTCCCGAGAAATCAGGC 430
QY 1327 CGCTTTTACGGGCTGGATTGTTACGCTGGGCTCCCATG 1365
DB 431 CGCTTTTACGGGCTGGATTGTTACGCTGGGCTCCCATG 469

Search completed: March 7, 2005, 22:56:52
Job time: 1102 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2005, 22:56:57 ; Search time 6339 seconds

(without alignments)
11379.049 Million cell updates/sec

Title: US-09-559-013e-23

Perfect score: 1895

Sequence: 1 gttagaggggctgtgtcc.....tggtagtttcaaaaaa 1895

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_hic.*
- 4: gb_est3.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_gsl.*
- 9: gb_gsl2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	766	40.4	1076	4	BM564020 AGENCOURT
2	755	39.8	1026	4	BM553910 AGENCOURT
3	754	39.8	1093	4	BM563837 AGENCOURT
4	753	39.7	1037	4	BM554354 AGENCOURT
5	734	38.7	836	4	BI830966 AGENCOURT
6	702	37.0	823	4	BI828365 AGENCOURT
7	682	36.0	1023	4	BM554310 AGENCOURT
8	678	35.8	1012	4	BM554519 AGENCOURT
9	676	35.7	779	4	BI829361 AGENCOURT
10	671	35.4	736	4	BI830145 AGENCOURT
11	670	35.4	827	4	BI820181 AGENCOURT
12	667	35.2	718	4	BI826973 AGENCOURT
13	666	35.1	769	4	BI820377 AGENCOURT
14	665	35.1	891	4	BI820136 AGENCOURT
15	655	34.6	706	4	BI820382 AGENCOURT
16	655	34.6	849	6	CD244111 AGENCOURT
17	651	34.4	847	4	BI829134 AGENCOURT
18	641	33.8	849	4	BI830306 AGENCOURT
19	640	33.8	737	4	BI829870 AGENCOURT
20	638	33.7	689	4	BI825892 AGENCOURT
21	620	32.7	866	4	BI828510 AGENCOURT
22	618	32.6	1029	4	BM560468 AGENCOURT
23	617	32.6	773	4	BG179727 AGENCOURT
24	614	32.4	753	4	BI829635 AGENCOURT

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26	603	32.1	1122	6	BM553134
27	595	31.8	886	6	CD243482
28	595	31.4	646	4	BI829508
29	591	31.2	762	4	BI463234
30	591	31.2	1074	4	BM563920 AGENCOURT
31	589	31.1	640	4	BI829306
32	589	31.1	855	4	BI561292
33	583	29.7	991	4	BI825474
34	562	29.7	658	4	BI828527
35	556	29.3	753	4	BG178214
36	554	29.2	675	4	BI520903
37	550	29.0	910	4	BI832341
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39	543	28.7	741	4	BG171883
40	541	28.5	909	4	BI827705
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42	534	28.2	591	5	BI115780
43	529	27.9	529	1	AI024421
44	527	27.8	610	6	CD694043
45	524	27.7	603	4	BI825890
46	498	26.3	919	4	BI828877
47	494	26.1	768	4	BI559547
48	488	25.8	755	4	BI831998
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50	477	25.2	841	4	BI906369
51	469	24.7	589	5	BP217972
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54	454	24.0	556	5	BP326362
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57	435	23.0	496	1	AA424694
58	433	22.8	825	4	BI825274
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60	425	22.4	762	4	BG171963
61	421	22.2	646	4	BI828554
62	412	21.7	518	1	AA864327
63	411	21.7	487	1	AA960777
64	395	20.8	800	5	BH852756
65	377	19.9	793	4	BI520735
66	361	19.1	412	1	AI126598
67	344	18.2	452	1	AI028208
68	339	17.9	370	1	AI575049
69	339	17.9	903	4	BI839130
70	337	17.8	400	1	AI131223
71	334	17.6	422	1	AI333624
72	334	17.6	422	1	AI333870
73	334	17.6	467	1	AI141116
74	334	17.6	579	4	BI829721
75	333	17.6	399	1	AI769240
76	325	17.2	478	1	AI125678
77	313	16.5	392	2	BF091360
78	312	16.5	807	4	BG171514
79	310	16.4	395	1	AI122673
80	308	16.3	421	1	AI091519
81	300	15.8	588	5	BP218002
82	296	15.6	354	1	AA406076
83	285	15.0	361	1	AA433593
84	284	15.0	363	1	AA709069
85	283	14.9	331	1	AI147148
86	269	14.2	376	7	R07741
87	227	12.0	471	1	AA993247
88	211	11.1	678	4	BI828257
89	205	10.8	831	4	BI520821
90	195	10.3	721	4	BI838009
91	190	10.0	310	1	AA471063
92	189	10.0	460	2	BF376156
93	174	9.2	426	1	AL597087
94	165	8.7	408	2	BF376146
95	162	8.5	162	1	AI382680
96	149	7.9	391	7	H30251
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99	114	6.0	173	1	A1574731	c 172	22	1.2	623	2	BE985980	BE985980
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101	95	5.0	277	1	A1138894	174	22	1.2	643	5	BM943116	BM943116
102	85	4.7	348	7	R07740	175	22	1.2	647	1	AV260707	AV260707
103	75	4.0	655	4	B1832428	176	22	1.2	664	6	CD768969	CD768969
104	70	3.7	651	1	B1830744	c 177	22	1.2	664	8	AO763048	AO763048
105	67	3.5	251	1	AA05433	178	22	1.2	669	6	CA465241	CA465241
106	57	3.0	1179	4	B1827945	179	22	1.2	673	2	BS541139	BS541139
107	54	2.8	386	2	AM948495	c 180	22	1.2	677	6	CA464922	CA464922
108	46	2.4	425	5	BX515014	181	22	1.2	694	5	BP770017	BP770017
109	46	2.4	627	1	AA154158	c 182	22	1.2	718	6	CD494137	CD494137
110	46	2.4	637	1	A1326707	c 183	22	1.2	749	9	CL660682	CL660682
111	41	2.1	445	2	B198626	184	22	1.2	767	7	CF739036	CF739036
112	40	2.2	577	2	BE232231	185	22	1.2	768	5	BX316397	BX316397
113	40	2.1	513	1	AL042116	186	22	1.2	788	5	BX316397	BX316397
114	39	2.1	310	5	BQ345731	187	22	1.2	799	5	BX316397	BX316397
115	38	2.0	489	4	BM256425	188	22	1.2	811	5	BX316397	BX316397
116	38	2.0	554	7	CK775903	189	22	1.2	814	6	CA464219	CA464219
117	35	1.8	432	4	BM5339243	190	22	1.2	827	5	BX316397	BX316397
118	35	1.8	450	4	BM5339243	191	22	1.2	938	5	BX316397	BX316397
119	35	1.8	611	4	BM5339243	192	22	1.2	1224	3	AK076691	AK076691
120	34	1.8	405	6	CB811133	193	22	1.2	1464	2	BF118779	BF118779
121	34	1.8	412	7	CR473065	194	22	1.2	3185	3	AK053586	AK053586
122	34	1.8	462	4	BI541194	c 195	22	1.2	31	1	AA621303	AA621303
123	33	1.7	115	1	AA992230	c 196	22	1.2	40	1	AI208979	AI208979
124	31	1.6	349	4	BM541067	197	21	1.1	211	9	CL478010	CL478010
125	31	1.6	417	1	A1573445	198	21	1.1	341	1	AA465568	AA465568
126	31	1.6	446	8	AQ024390	199	21	1.1	399	2	AM630546	AM630546
127	31	1.6	533	7	CO607922	c 200	21	1.1	407	2	AM630546	AM630546
128	31	1.6	575	7	CO597003	c 201	21	1.1	452	2	BF723770	BF723770
129	31	1.6	584	7	CO595610	c 202	21	1.1	452	9	CL873583	CL873583
130	31	1.6	615	7	CO595171	c 203	21	1.1	475	8	AZ170397	AZ170397
131	31	1.6	623	7	CO601955	c 204	21	1.1	475	1	AA640562	AA640562
132	31	1.6	719	9	CE286339	c 205	21	1.1	497	2	BF443476	BF443476
133	29	1.5	582	4	BM537627	c 206	21	1.1	513	2	BE223089	BE223089
134	26	1.4	306	7	CO604503	c 207	21	1.1	550	4	BI679826	BI679826
135	26	1.4	758	7	CK469251	c 208	21	1.1	563	1	AI300103	AI300103
136	26	1.4	770	7	CK598900	c 209	21	1.1	563	1	AI743822	AI743822
137	26	1.4	792	8	BZ226260	c 210	21	1.1	568	5	BM968328	BM968328
138	26	1.4	797	7	CK604050	c 211	21	1.1	582	8	AZ337449	AZ337449
139	26	1.4	836	7	CK598106	c 212	21	1.1	601	1	AL674723	AL674723
140	26	1.4	857	7	CK471040	c 213	21	1.1	607	1	AL896981	AL896981
141	24	1.3	358	8	AZ846675	c 214	21	1.1	610	4	BG491920	BG491920
142	24	1.3	369	5	BY061518	215	21	1.1	636	7	CM075310	CM075310
143	24	1.3	647	8	AZ359345	c 216	21	1.1	639	5	BQ015325	BQ015325
144	23	1.2	564	2	BE111104	c 217	21	1.1	647	5	BX267049	BX267049
145	23	1.2	634	2	BE111012	c 218	21	1.1	647	5	BX267049	BX267049
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147	23	1.2	695	1	AV092095	c 220	21	1.1	667	5	BX267049	BX267049
148	23	1.2	725	5	BM950309	c 221	21	1.1	667	5	BX267049	BX267049
149	23	1.2	792	7	CK595043	c 222	21	1.1	667	5	BX267049	BX267049
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151	22	1.2	179	2	AW188855	c 224	21	1.1	667	5	BX267049	BX267049
152	22	1.2	239	2	BF152647	c 225	21	1.1	667	5	BX267049	BX267049
153	22	1.2	251	7	CK896663	c 226	21	1.1	667	5	BX267049	BX267049
154	22	1.2	282	2	BS574057	c 227	21	1.1	667	5	BX267049	BX267049
155	22	1.2	266	2	BS564350	c 228	21	1.1	667	5	BX267049	BX267049
156	22	1.2	306	7	CF104508	c 229	21	1.1	667	5	BX267049	BX267049
157	22	1.2	331	2	BE046182	c 230	21	1.1	667	5	BX267049	BX267049
158	22	1.2	363	5	BY093354	c 231	21	1.1	667	5	BX267049	BX267049
159	22	1.2	368	5	BY099028	c 232	21	1.1	667	5	BX267049	BX267049
160	22	1.2	371	5	BP770016	c 233	21	1.1	667	5	BX267049	BX267049
161	22	1.2	416	2	BF021888	c 234	21	1.1	667	5	BX267049	BX267049
162	22	1.2	422	2	BF149695	c 235	21	1.1	667	5	BX267049	BX267049
163	22	1.2	459	4	BM288266	c 236	21	1.1	667	5	BX267049	BX267049
164	22	1.2	470	9	CR262336	c 237	21	1.1	667	5	BX267049	BX267049
165	22	1.2	511	1	AV005781	c 238	21	1.1	667	5	BX267049	BX267049
166	22	1.2	517	1	A1553526	c 239	21	1.1	667	5	BX267049	BX267049
167	22	1.2	523	9	CR138551	c 240	21	1.1	667	5	BX267049	BX267049
168	22	1.2	544	8	AZ252213	c 241	21	1.1	667	5	BX267049	BX267049
169	22	1.2	570	9	CE671990	c 242	21	1.1	667	5	BX267049	BX267049
170	22	1.2	579	7	CF157497	c 243	21	1.1	667	5	BX267049	BX267049

244	21	1.1	948	5	BX394390	BX394390	BX394390	C 317	20	1.1	413	2	BB740843	BB740843	BB740843	BB740843
245	21	1.1	958	1	AL562857	AL562857	AL562857	C 318	20	1.1	425	6	BY692699	BY692699	BY692699	BY692699
246	21	1.1	979	5	EX458436	EX458436	EX458436	C 319	20	1.1	426	1	AV808145	AV808145	AV808145	AV808145
247	21	1.1	991	5	BQ072169	AGENCOURT	BQ072169	C 320	20	1.1	426	5	BY283318	BY283318	BY283318	BY283318
248	21	1.1	992	4	BM558887	AGENCOURT	BM558887	C 321	20	1.1	429	1	AA162353	AA162353	AA162353	AA162353
249	21	1.1	1001	2	BF689251	602185042	BF689251	C 322	20	1.1	432	6	BY693848	BY693848	BY693848	BY693848
250	21	1.1	1005	5	EX399152	BX399152	EX399152	C 323	20	1.1	433	8	CC016767	PUECWO4TD	CC016767	PUECWO4TD
251	21	1.1	1015	5	BX394389	BX394389	BX394389	C 324	20	1.1	434	6	BY579732	BY579732	BY579732	BY579732
252	21	1.1	1018	5	EX375576	BX375576	EX375576	C 325	20	1.1	435	6	BY579732	BY579732	BY579732	BY579732
253	21	1.1	1022	1	AL567135	AL567135	AL567135	C 326	20	1.1	438	5	BY030987	BY030987	BY030987	BY030987
254	21	1.1	1030	1	AL580458	AL580458	AL580458	C 327	20	1.1	438	9	CL952245	O6JRU000	CL952245	O6JRU000
255	21	1.1	1060	8	CC272654	CH261-121	CC272654	C 328	20	1.1	441	6	BY548394	BY548394	BY548394	BY548394
256	21	1.1	1070	4	BM557214	AGENCOURT	BM557214	C 329	20	1.1	442	9	AG192277	Pan t10gl	AG192277	Pan t10gl
257	21	1.1	1072	1	AL562840	AL562840	AL562840	C 330	20	1.1	443	5	BP618329	BP618329	BP618329	BP618329
258	21	1.1	1077	5	EX446398	EX446398	EX446398	C 331	20	1.1	445	6	BY532172	BY532172	BY532172	BY532172
259	21	1.1	1108	1	AL539134	AL539134	AL539134	C 332	20	1.1	446	2	BB785776	BB785776	BB785776	BB785776
260	21	1.1	1106	5	BX358634	BX358634	BX358634	C 333	20	1.1	448	2	BB779924	BB779924	BB779924	BB779924
261	21	1.1	1144	4	BM554390	AGENCOURT	BM554390	C 334	20	1.1	449	9	AG198077	Pan t10gl	AG198077	Pan t10gl
262	21	1.1	1153	5	BM911580	AGENCOURT	BM911580	C 335	20	1.1	453	1	AV791304	AV791304	AV791304	AV791304
263	21	1.1	1165	5	BM916435	AGENCOURT	BM916435	C 336	20	1.1	454	7	CR756533	CR756533	CR756533	CR756533
264	21	1.1	1256	3	CR610727	full-leng	CR610727	C 337	20	1.1	454	7	CR757049	CR757049	CR757049	CR757049
265	21	1.1	1679	3	AF113672	Homo sapi	AF113672	C 338	20	1.1	454	7	CR757052	CR757052	CR757052	CR757052
266	21	1.1	1734	3	CR594170	full-leng	CR594170	C 339	20	1.1	454	7	CR757267	CR757267	CR757267	CR757267
267	20	1.1	138	2	BF399123	UI-R-CAL-	BF399123	C 340	20	1.1	454	7	CR757779	CR757779	CR757779	CR757779
268	20	1.1	187	1	AI125674	q90905.x	AI125674	C 341	20	1.1	454	7	CR757782	CR757782	CR757782	CR757782
269	20	1.1	194	2	BF309565	BF309565	BF309565	C 342	20	1.1	456	2	BF403476	UI-R-CAL-	BF403476	UI-R-CAL-
270	20	1.1	208	7	CF159511	B0673B09-	CF159511	C 343	20	1.1	458	6	BY570154	BY570154	BY570154	BY570154
271	20	1.1	233	9	CG410901	TP2D0017	CG410901	C 344	20	1.1	464	6	C98732	C98732	C98732	C98732
272	20	1.1	235	1	AV381063	AV381063	AV381063	C 345	20	1.1	467	1	AI840282	UI-M-AH0-	AI840282	UI-M-AH0-
273	20	1.1	246	2	AW860616	QVO-CT038	AW860616	C 346	20	1.1	467	2	BE228381	98AS1781	BE228381	98AS1781
274	20	1.1	256	9	CE635060	t1gr-g88-	CE635060	C 347	20	1.1	470	8	BH841392	TC3-51L6.	BH841392	TC3-51L6.
275	20	1.1	275	2	BE3354005	BE3354005	BE3354005	C 348	20	1.1	470	8	BH842177	TC3-51L6.	BH842177	TC3-51L6.
276	20	1.1	285	2	BB311479	BB311479	BB311479	C 349	20	1.1	470	8	BH859000	S5_176a_s	BH859000	S5_176a_s
277	20	1.1	292	2	BB434848	BB434848	BB434848	C 350	20	1.1	471	1	AV440874	AV440874	AV440874	AV440874
278	20	1.1	294	2	BB302012	BB302012	BB302012	C 351	20	1.1	476	2	BF399890	UI-R-CAL-	BF399890	UI-R-CAL-
279	20	1.1	295	2	BB192935	BB192935	BB192935	C 352	20	1.1	482	1	AA270689	AA270689	AA270689	AA270689
280	20	1.1	295	2	BB262387	BB262387	BB262387	C 353	20	1.1	483	4	BM106701	510637 MA	BM106701	510637 MA
281	20	1.1	296	2	BB087518	BB087518	BB087518	C 354	20	1.1	499	1	AA549047	AA549047	AA549047	AA549047
282	20	1.1	298	2	BB310445	BB310445	BB310445	C 355	20	1.1	501	1	AA672243	V112b10.i.r	AA672243	V112b10.i.r
283	20	1.1	299	2	BB222595	BB222595	BB222595	C 356	20	1.1	508	8	AZ846524	2M0146F13	AZ846524	2M0146F13
284	20	1.1	303	1	AV044452	AV044452	AV044452	C 357	20	1.1	510	8	BH025702	RPCI-24-1	BH025702	RPCI-24-1
285	20	1.1	306	1	AV146700	AV146700	AV146700	C 358	20	1.1	516	2	BE652261	UI-M-AH0-	BE652261	UI-M-AH0-
286	20	1.1	308	2	BB450098	BB450098	BB450098	C 359	20	1.1	517	1	AI648160	uk39e09.x	AI648160	uk39e09.x
287	20	1.1	312	5	BY128622	BY128622	BY128622	C 360	20	1.1	520	7	CO711738	DG14-1751	CO711738	DG14-1751
288	20	1.1	314	2	BB508248	BB508248	BB508248	C 361	20	1.1	521	6	CA395411	cs64b07.y	CA395411	cs64b07.y
289	20	1.1	316	2	BB311384	BB311384	BB311384	C 362	20	1.1	521	8	B95191	CIT-HSP-216	B95191	CIT-HSP-216
290	20	1.1	320	2	BB220475	BB220475	BB220475	C 363	20	1.1	526	8	AY127380	AY127380	AY127380	AY127380
291	20	1.1	321	2	BB218513	BB218513	BB218513	C 364	20	1.1	539	7	T46807	10070 Lambd	T46807	10070 Lambd
292	20	1.1	323	2	BB319094	BB319094	BB319094	C 365	20	1.1	539	9	CL355340	RPCI144_40	CL355340	RPCI144_40
293	20	1.1	326	1	AA198159	mv46c07.i.r	AA198159	C 366	20	1.1	541	6	CD804541	UI-M-GV0-	CD804541	UI-M-GV0-
294	20	1.1	326	5	BB315971	BB315971	BB315971	C 367	20	1.1	542	2	BB821344	BB821344	BB821344	BB821344
295	20	1.1	326	5	BP427995	BP427995	BP427995	C 368	20	1.1	544	4	BM502825	ii44f03.x	BM502825	ii44f03.x
296	20	1.1	328	6	CA960692	TGEStzyl	CA960692	C 369	20	1.1	547	2	BB767095	BB767095	BB767095	BB767095
297	20	1.1	329	1	AI849070	UI-M-AH1-	AI849070	C 370	20	1.1	551	5	BP370198	BP370198	BP370198	BP370198
298	20	1.1	329	2	BB320304	BB320304	BB320304	C 371	20	1.1	551	6	CB259324	59-E9623-	CB259324	59-E9623-
299	20	1.1	330	2	BB551533	BB551533	BB551533	C 372	20	1.1	552	1	AJ801501	AJ801501	AJ801501	AJ801501
300	20	1.1	345	5	BB629749	BB629749	BB629749	C 373	20	1.1	556	1	AV562174	AV562174	AV562174	AV562174
301	20	1.1	347	1	AA204081	mu26g01.i.r	AA204081	C 374	20	1.1	558	4	BI420420	BI420420	BI420420	BI420420
302	20	1.1	350	1	AI006481	ua73QD09.i.r	AI006481	C 375	20	1.1	558	4	BI420550	LjN5T57a	BI420550	LjN5T57a
303	20	1.1	356	1	AA143967	mq53F09.i.r	AA143967	C 376	20	1.1	572	1	AV533224	AV533224	AV533224	AV533224
304	20	1.1	364	5	BY415972	BY415972	BY415972	C 377	20	1.1	572	5	BQ552867	H4018F11-	BQ552867	H4018F11-
305	20	1.1	380	5	BY154810	BY154810	BY154810	C 378	20	1.1	574	4	BI593579	RH11689.5	BI593579	RH11689.5
306	20	1.1	383	1	AU040498	AU040498	AU040498	C 379	20	1.1	581	9	CE471060	t1gr-g8s-	CE471060	t1gr-g8s-
307	20	1.1	387	5	EX440108	EX440108	EX440108	C 380	20	1.1	588	5	BU219309	603756701	BU219309	603756701
308	20	1.1	390	2	BF399015	UI-R-CAL-	BF399015	C 381	20	1.1	589	8	BH334793	CH230-168	BH334793	CH230-168
309	20	1.1	393	6	BY684146	BY684146	BY684146	C 382	20	1.1	590	5	BQ445107	UI-M-ER0-	BQ445107	UI-M-ER0-
310	20	1.1	394	8	AQ074596	CIT-HSP-2	AQ074596	C 383	20	1.1	591	9	CR139899	Forward s	CR139899	Forward s
311	20	1.1	399	2	BB741438	BB741438	BB741438	C 384	20	1.1	595	1	AI648096	uk42c02.x	AI648096	uk42c02.x
312	20	1.1	400	5	BY523060	BY523060	BY523060	C 385	20	1.1	606	2	AW584044	100000010	AW584044	100000010
313	20	1.1	404	5	BY521869	BY521869	BY521869	C 386	20	1.1	611	2	BF466965	UI-M-CG0P	BF466965	UI-M-CG0P
314	20	1.1	407	5	BY437543	BY437543	BY437543	C 387	20	1.1	613	8	BH521075	BOGMP75TR	BH521075	BOGMP75TR
315	20	1.1	408	1	AU041562	AU041562	AU041562	C 388	20	1.1	615	8	AZ618875	1M0450L17	AZ618875	1M0450L17
316	20	1.1	411	6	BY613336	BY613336	BY613336	C 389	20	1.1	619	5	BU383085	603582103	BU383085	603582103

C 390	20	1.1	624	4	BI617619	BI617619 RH48011.5	C 463	19	1.0	286	1	AV009586
C 391	20	1.1	626	5	BU207876	BU207876 604156159	C 464	19	1.0	289	8	BH226730
C 392	20	1.1	628	9	CE207792	CE207792 tigr-gss-	C 465	19	1.0	296	7	T01789
C 393	20	1.1	630	2	BH226025	BH226025 BH226025	C 466	19	1.0	300	1	AV177811
C 394	20	1.1	630	5	BP132780	BP132780 BP132780	C 467	19	1.0	300	1	AV177811
C 395	20	1.1	633	1	AV783144	AV783144 AV783144	C 468	19	1.0	300	1	AV177811
C 396	20	1.1	636	6	BY724479	BY724479 BY724479	C 469	19	1.0	303	4	BI399942
C 397	20	1.1	645	1	AI790218	AI790218 UK57D03.X	C 470	19	1.0	308	1	BI399942
C 398	20	1.1	652	4	BJ089214	BJ089214 BJ089214	C 471	19	1.0	309	9	CL406443
C 399	20	1.1	652	7	CN524895	CN524895 UI-M-GHO-	C 472	19	1.0	311	9	CE220476
C 400	20	1.1	662	5	BM949032	BM949032 UI-M-GHO-	C 473	19	1.0	321	1	AL046395
C 401	20	1.1	662	5	BM949032	BM949032 UI-M-GHO-	C 474	19	1.0	326	4	BI347814
C 402	20	1.1	670	6	CL321038	CL321038 CH242.15E	C 475	19	1.0	329	5	BY191577
C 403	20	1.1	675	9	CC482231	CC482231 UI-M-GVO-	C 476	19	1.0	332	2	BH312074
C 404	20	1.1	678	6	CD774482	CD774482 UI-M-AQO-	C 477	19	1.0	332	7	CA466874
C 405	20	1.1	681	1	AI788958	AI788958 UK56B09.X	C 478	19	1.0	336	2	BH645761
C 406	20	1.1	684	1	AI547206	AI547206 PN3.1.02	C 479	19	1.0	337	2	BF193883
C 407	20	1.1	702	7	CF532249	CF532249 UI-M-GHO-	C 480	19	1.0	339	1	AI242332
C 408	20	1.1	704	5	BU260507	BU260507 603504760	C 481	19	1.0	343	8	B2955950
C 409	20	1.1	704	5	BU260507	BU260507 603504760	C 482	19	1.0	344	9	CL411414
C 410	20	1.1	707	8	BZ425814	BZ425814 BOPR87TF	C 483	19	1.0	349	2	BF857129
C 411	20	1.1	708	5	BQ552868	BQ552868 BOPR87TF	C 484	19	1.0	351	1	AI565157
C 412	20	1.1	709	6	BY761465	BY761465 BOPR87TF	C 485	19	1.0	358	9	TA98A09P
C 413	20	1.1	719	5	BU222881	BU222881 603798242	C 486	19	1.0	360	1	AV194747
C 414	20	1.1	728	9	CE017102	CE017102 tigr-gss-	C 487	19	1.0	360	1	AV201267
C 415	20	1.1	741	5	BU228653	BU228653 603495045	C 488	19	1.0	363	8	BH064023
C 416	20	1.1	744	5	BU140329	BU140329 603134014	C 489	19	1.0	372	2	BH925075
C 417	20	1.1	753	7	CF744376	CF744376 UI-M-GVO-	C 490	19	1.0	372	9	EX973961
C 418	20	1.1	754	5	BU327772	BU327772 603494529	C 491	19	1.0	372	9	CR068837
C 419	20	1.1	766	8	BZ436444	BZ436444 BONIB41TR	C 492	19	1.0	373	1	AI659595
C 420	20	1.1	774	5	BU386518	BU386518 603856722	C 493	19	1.0	373	2	BF222225
C 421	20	1.1	778	7	CO421662	CO421662 GGEZHT102	C 494	19	1.0	378	1	AA201535
C 422	20	1.1	783	9	CS581875	CS581875 tigr-gss-	C 495	19	1.0	378	1	AV189263
C 423	20	1.1	785	6	CS954150	CS954150 AGENCOURT	C 496	19	1.0	380	5	BU810799
C 424	20	1.1	794	8	AQ746766	AQ746766 HS.2276.A	C 497	19	1.0	383	4	BG319017
C 425	20	1.1	796	7	CF204292	CF204292 R8909151	C 498	19	1.0	383	8	BH65804
C 426	20	1.1	803	5	BU383161	BU383161 603583126	C 499	19	1.0	385	4	BI001198
C 427	20	1.1	808	7	CK119755	CK119755 201C15.P1	C 500	19	1.0	387	2	BF359967
C 428	20	1.1	817	8	BZ448909	BZ448909 BONPS12TR	C 501	19	1.0	391	1	AU219437
C 429	20	1.1	832	8	BZ174367	BZ174367 CH230-268	C 502	19	1.0	393	4	BU146916
C 430	20	1.1	843	9	CL658114	CL658114 PRI0130b	C 503	19	1.0	395	1	AA523230
C 431	20	1.1	850	9	CNS04L1L	CL295554 Tetraodon	C 504	19	1.0	400	6	BY603807
C 432	20	1.1	881	5	BU231563	BU231563 603796517	C 505	19	1.0	401	1	AI047576
C 433	20	1.1	888	1	AU079261	AU079261 AU079261	C 506	19	1.0	401	1	AI047576
C 434	20	1.1	912	7	CF518026	CF518026 CAP0006.1	C 507	19	1.0	402	9	CE181843
C 435	20	1.1	937	6	CD779104	CD779104 EST650465	C 508	19	1.0	403	1	AL024186
C 436	20	1.1	945	9	BG847974	BG847974 1024019H1	C 509	19	1.0	403	4	BG318830
C 437	20	1.1	951	6	CD796981	CD796981 AGENCOURT	C 510	19	1.0	406	1	AX098302
C 438	20	1.1	960	5	BU515004	BU515004 AGENCOURT	C 511	19	1.0	408	4	BG319141
C 439	20	1.1	965	8	AZ191212	AZ191212 SP.1019.A	C 512	19	1.0	408	7	CO306669
C 440	20	1.1	985	8	CC210107	CC210107 CH261-101	C 513	19	1.0	409	1	AV747267
C 441	20	1.1	1028	8	CC241708	CC241708 CH261-102	C 514	19	1.0	411	1	AI034081
C 442	20	1.1	1091	9	CL049907	CL049907 CH216-71F	C 515	19	1.0	414	6	CB801904
C 443	20	1.1	1100	4	BG112285	BG112285 602282431	C 516	19	1.0	415	9	CE065111
C 444	20	1.1	1261	8	AG322847	AG322847 Pan trogl	C 517	19	1.0	418	1	AI190885
C 445	20	1.1	1292	9	AC163602	AC163602 TAM32-32K	C 518	19	1.0	420	4	BA966069
C 446	20	1.1	1363	3	CNS09ZCT	NS831290 Arabidops	C 519	19	1.0	424	8	BE200434
C 447	20	1.1	1472	3	AK007700	AK007700 Mus muscu	C 520	19	1.0	429	2	CF803743
C 448	20	1.1	1530	3	AK048151	AK048151 1024020H0	C 521	19	1.0	430	2	BF83014
C 449	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 522	19	1.0	432	7	BE950133
C 450	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 523	19	1.0	432	2	BE950133
C 451	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 524	19	1.0	432	7	BE950133
C 452	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 525	19	1.0	432	8	BH031276
C 453	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 526	19	1.0	434	4	BG526928
C 454	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 527	19	1.0	435	4	BG625790
C 455	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 528	19	1.0	435	4	BH119185
C 456	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 529	19	1.0	435	4	BH119185
C 457	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 530	19	1.0	435	4	BH119185
C 458	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 531	19	1.0	435	4	BH119185
C 459	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 532	19	1.0	435	4	BH119185
C 460	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 533	19	1.0	435	4	BH119185
C 461	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 534	19	1.0	435	4	BH119185
C 462	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 535	19	1.0	435	4	BH119185

C 536	19	1.0	436	1	AA089129	AA089129	ml57h08.r	609	19	1.0	551	4	BG317960	BG317960	NPXPV_007
C 537	19	1.0	439	4	BG039896	NXSI_105	C 610	19	1.0	555	5	AA530375	AA530375	VJ48C05.i	
C 538	19	1.0	444	7	CO191078	EX050644.i	C 611	19	1.0	556	5	BX515394	BX515394	SD07205.3	
C 539	19	1.0	446	1	AA221606	mw50a02.i	612	19	1.0	557	4	BG639831	BG639831	SD07205.3	
C 540	19	1.0	446	2	BE997181	NXCI_107	613	19	1.0	558	1	AI455519	AI455519	LD24677.3	
C 541	19	1.0	447	1	AI315118	u129b08.x	614	19	1.0	559	8	AO471138	AO471138	CITBI-E1	
C 542	19	1.0	449	1	AA599011	ae41e10.s	615	19	1.0	560	8	AO700627	AO700627	HS_5379.A	
C 543	19	1.0	449	5	BQ696718	NPXPV_045	C 616	19	1.0	561	9	CR109242	CR109242	Forward.s	
C 544	19	1.0	450	1	AI174037	u675a01.x	617	19	1.0	562	4	BG546447	BG546447	602573790	
C 545	19	1.0	452	4	BW764395	K-EST0045	C 618	19	1.0	562	8	AZ983482	AZ983482	2M0264108	
C 546	19	1.0	454	1	AI681144	tx44d11.x	C 619	19	1.0	564	4	BI331414	BI331414	602981711	
C 547	19	1.0	454	7	CO303130	EX240122.i	C 620	19	1.0	564	8	BH274165	BH274165	CH230-35C	
C 548	19	1.0	456	1	AA250480	m259f03.r	C 621	19	1.0	569	5	BQ490376	BQ490376	92-E9437-	
C 549	19	1.0	456	7	CO331763	EX301638.s	C 622	19	1.0	570	4	BI122426	BI122426	1006P61P	
C 550	19	1.0	458	6	BY530685	BY530685	C 623	19	1.0	571	5	BUE96780	BUE96780	LI2in1313	
C 551	19	1.0	459	5	EX255067	EX255067	C 624	19	1.0	575	1	AI511712	AI511712	LI43204.5	
C 552	19	1.0	461	2	BF510029	UI-H-B14	C 625	19	1.0	579	7	CR904083	CR904083	1e72e06.x	
C 553	19	1.0	461	4	BI805021	SO03G10.S	C 626	19	1.0	580	7	CF793841	CF793841	889290.MA	
C 554	19	1.0	469	6	CB679745	QJNBF03K	C 627	19	1.0	582	5	BP206022	BP206022	BP206022	
C 555	19	1.0	472	6	CA657032	w1m0.pk00	C 628	19	1.0	582	5	BP313328	BP313328	BP313328	
C 556	19	1.0	475	7	CN311053	170006002	C 629	19	1.0	582	9	CG986652	CG986652	CH240_157	
C 557	19	1.0	477	1	AJ654960	AJ654960	C 630	19	1.0	582	9	CL337635	CL337635	RPC144_26	
C 558	19	1.0	481	8	AQ524247	HS_5234.B	C 631	19	1.0	585	1	AI315057	AI315057	u128h06.x	
C 559	19	1.0	483	4	BI359750	384416.MA	C 632	19	1.0	589	1	AU213220	AU213220	AU213220	
C 560	19	1.0	486	1	AA816758	LD08464.5	C 633	19	1.0	589	4	BI165134	BI165134	RE04956.5	
C 561	19	1.0	486	7	CF792480	885418.MA	C 634	19	1.0	592	9	BI154152	BI154152	Danio rer	
C 562	19	1.0	489	1	AI804518	tp60c07.x	C 635	19	1.0	594	2	BE444330	BE444330	WHE1117.H	
C 563	19	1.0	490	9	CE129461	tigr-g88-	C 636	19	1.0	595	4	BI374587	BI374587	R62221.5	
C 564	19	1.0	491	1	AI480764	AI480764.v129a09.x	C 637	19	1.0	597	8	CC417598	CC417598	PUHOA8TD	
C 565	19	1.0	491	9	AA439254	LD13766.5	C 638	19	1.0	599	1	AV668373	AV668373	AV668373	
C 566	19	1.0	491	9	CL198609	ZMMBEC007	C 639	19	1.0	600	6	CA776531	CA776531	ip06d01.y	
C 567	19	1.0	492	8	AZ246758	RPCI-23-7	C 640	19	1.0	601	1	AA392719	AA392719	LD11833.5	
C 568	19	1.0	492	9	CC961058	BOICL58TR	C 641	19	1.0	601	9	CE374645	CE374645	tigr-g88-	
C 569	19	1.0	493	4	BI403264	MI-P-CPI-	C 642	19	1.0	603	1	AA950740	AA950740	LD30848.5	
C 570	19	1.0	494	4	BI364519	RE49660.5	C 643	19	1.0	603	1	AA392383	AA392383	LD11236.5	
C 571	19	1.0	494	7	CO239216	WS00725.B	C 644	19	1.0	603	9	CE378818	CE378818	tigr-g88-	
C 572	19	1.0	496	8	AZ921202	1006024G1	C 645	19	1.0	604	7	CO473667	CO473667	G000410.B	
C 573	19	1.0	498	2	BE138353	u51f08.y	C 646	19	1.0	606	6	CA037844	CA037844	HFGI829.H	
C 574	19	1.0	500	9	CR503318	Medicago	C 647	19	1.0	610	8	AZ382187	AZ382187	IM0139D07	
C 575	19	1.0	502	4	BI643835	NPXPV_123	C 648	19	1.0	611	7	CR369651	CR369651	CR369651	
C 576	19	1.0	504	7	CF430686	NIT1_3.D0	C 649	19	1.0	611	8	B94389	B94389	CIT-HSP-217	
C 577	19	1.0	506	2	BF733385	MR1-AN003	C 650	19	1.0	617	7	CK528231	CK528231	rswfao.00	
C 578	19	1.0	506	8	AO373107	RPCI11-14	C 651	19	1.0	617	7	CK998658	CK998658	ip34c11.b	
C 579	19	1.0	507	7	CN335823	CN335823	C 652	19	1.0	619	4	BJ498602	BJ498602	BX498602	
C 580	19	1.0	508	1	AI315315	u137b02.x	C 653	19	1.0	620	5	BX984555	BX984555	BX984555	
C 581	19	1.0	509	4	BG039820	NXSI_101	C 654	19	1.0	620	7	CO42975	CO42975	WS0032.B2	
C 582	19	1.0	512	8	AZ001768	CD214726	C 655	19	1.0	620	8	AZ166858	AZ166858	SP_0094.A	
C 583	19	1.0	518	6	CD214726	pgm2n.pk0	C 656	19	1.0	620	9	CE502502	CE502502	tigr-g88-	
C 584	19	1.0	519	4	BI483810	RE66759.5	C 657	19	1.0	621	4	BJ104712	BJ104712	BJ104712	
C 585	19	1.0	519	9	CC623040	OGWHM65TV	C 658	19	1.0	623	7	CK529240	CK529240	rswfao.00	
C 586	19	1.0	523	4	BG496637	BG149637.nad31f03.	C 659	19	1.0	624	7	CV031738	CV031738	RTNACLI_3	
C 587	19	1.0	524	4	BI173716	RE16805.5	C 660	19	1.0	624	8	BZ944337	BZ944337	CH240_83C	
C 588	19	1.0	524	4	BI374007	RE61506.5	C 661	19	1.0	625	8	AZ210619	AZ210619	SP_0154.A	
C 589	19	1.0	525	1	AI877402	AI877402.v74c06.r	C 662	19	1.0	626	7	CF175766	CF175766	795758.MA	
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C 592	19	1.0	529	9	CE152472	Medicago	C 665	19	1.0	627	9	CG453622	CG453622	OGTCA76TV	
C 593	19	1.0	529	9	CE145466	CE145466.tigr-g88-	C 666	19	1.0	634	4	BG524191	BG524191	39-89.Ste	
C 594	19	1.0	530	8	AQ522658	AQ522658.HS_5208.B	C 667	19	1.0	636	5	BU695976	BU695976	Pan trogl	
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C 596	19	1.0	532	8	AZ716224	RPCI-24-1	C 669	19	1.0	636	9	CG067448	CG067448	PUIOC68TD	
C 597	19	1.0	534	4	BI116652	602868329	C 670	19	1.0	637	1	AI518028	AI518028	LD37429.5	
C 598	19	1.0	535	2	BF273102	GA_EB001	C 671	19	1.0	637	8	AZ166781	AZ166781	SP_0094.A	
C 599	19	1.0	537	4	BI126439	IO75P43P	C 672	19	1.0	637	9	CE172594	CE172594	tigr-g88-	
C 600	19	1.0	538	1	AL922732	AL922732	C 673	19	1.0	638	2	BB607654	BB607654	BB607654	
C 601	19	1.0	543	7	CF480542	POLL_66.H	C 674	19	1.0	640	1	AI511849	AI511849	LD43388.5	
C 602	19	1.0	544	7	CF480542	POLL_66.H	C 675	19	1.0	640	4	BM153404	BM153404	TCBAP2D11	
C 603	19	1.0	545	7	CN233217	CN233217	C 676	19	1.0	640	5	BQ780302	BQ780302	UI-R-FFO-	
C 604	19	1.0	546	4	BI348699	ic67907.x	C 677	19	1.0	642	8	AZ210120	AZ210120	SP_0155.A	
C 605	19	1.0	547	1	AI515163	LD46871.5	C 678	19	1.0	642	9	BX991288	BX991288	Forward.s	
C 606	19	1.0	547	1	AV833182	AV833182	C 679	19	1.0	643	4	BI214360	BI214360	RE20138.5	
C 607	19	1.0	548	7	CF489891	POLL_61.F	C 680	19	1.0	646	8	AZ203691	AZ203691	SP_0084.A	
C 608	19	1.0	550	9	CE626093	CE626093.tigr-g88-	C 681	19	1.0	647	1	AV344893	AV344893	AV344893	


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974      18      0.9      247      1      AV324605
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c 977      18      0.9      250      2      BF198866
978      18      0.9      251      8      BH885353
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980      18      0.9      253      7      CR557267
c 981      18      0.9      254      7      CE643735
982      18      0.9      255      2      AW872590
c 983      18      0.9      256      7      CK767555
c 984      18      0.9      257      1      AE632496
c 985      18      0.9      258      7      CO229696
c 986      18      0.9      259      2      BE672130
c 987      18      0.9      260      6      CB485950
c 988      18      0.9      261      6      CB490595
c 989      18      0.9      262      1      AL642961
c 990      18      0.9      263      5      BP951301
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c 992      18      0.9      265      7      CO320178
c 993      18      0.9      266      1      AE676301
c 994      18      0.9      267      2      BE938535
c 995      18      0.9      268      1      AE668196
c 996      18      0.9      269      2      BE324310
c 997      18      0.9      270      9      AG266519
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ALIGNMENTS

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RESULT 1
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LOCUS      AGENCOURT 6560257 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742040
5', mRNA sequence.
ACCESSION      BM564020.1 GI:18811457
VERSION      EST.
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1076)
AUTHORS      NIH-MGC http://mgs.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
      Email: cgapbs-remail.nih.gov
      Tissue Procurement: Life Technologies, Inc.
      cDNA Library Preparation: Life Technologies, Inc.
      DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
      DNA Sequencing by: Agencourt Bioscience Corporation
      Clone distribution: MGC clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at:
      http://image.llnl.gov
      Plate: L1AM12759 row: i column: 17
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          anonymous male age 27. Library is oligo-dT primed and
          directionally cloned (EcoRV site is destroyed upon
          cloning). Average insert size 1.3 kb, insert size range

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FEATURES

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ORIGIN
Query Match      40.4%; Score 766; DB 4; Length 1076;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      142      CCACCTCCAGGAGCCCTCTCTCTCTACCGAATACGAACGCTTCTTTCGCACTGCTGACT 201
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QY      202      CCAACCTGGAAGGAGAGACTACCTGCGCTCTCGTGGAACCCACAGCTCCCGGAATCCC 261
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QY      262      ACCTCTGTCAGCTGGACCAATATGAAAAACACAGGCTTAGTGCCGATGGTGTCTGTC 321
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QY      322      TCGAACCTCCCTTATGCTCTCTGTTGAGTCTTTCGCACTTCACTCACTACCTGTC 381
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QY      382      TCCAAACACGCTACTATGCAAGAGAGTCTCTGTTTCCAGCAGCTCTCTATTCTCTCA 441
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QY      442      CTTAACTCTCTAAGGAGATAGAAGTTTCACTGTAAGTCTCACCCACCAAGATGACCTCC 501
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DB      501      CCCATCTCACCCCACTTTCACAGTGACAGAACCCAGCCTTCCAGCCCTGGCTGAGAGG 560
QY      562      CTGAGCAACAACTGGAAGAGTCTTCACTTCTCTTCTGAGGAGCCAGGAGCA 621
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QY      622      GCGCCAGAGCACAGGAGGAGGAGTGGAGCAGGAGGAGCCGAGGAGCCGAGCAAGAAC 681
DB      621      GCGCCAGAGCACAGGAGGAGGAGGAGTGGAGCAGGAGGAGCCGAGGAGCCGAGCAAGAAC 680
QY      682      AGCAGGAAGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 741
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QY      742      CAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 801
DB      741      CAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 800
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DB      801      TCAGAGCCCAAGTTTCACTCTGAAATCTCTATCTCTTA 837

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RESULT 2
BM553910
LOCUS      AGENCOURT 6546785 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742226
5', mRNA sequence.
ACCESSION      BM553910

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VERSION BM53910.1 GI:18793058
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1026)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Site 2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

ORIGIN
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 805; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB |||||||
QY 61 GCGCTGGCTTCTTCCCTCCTCTGAGGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB |||||||
QY 65 GCGCTGGCTTCTTCCCTCCTCTGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 124
DB |||||||
QY 121 GCCCAGGATTCGACTCAGCGCCCTCTCCAGGCGGCTCTCTCTCTACCGAATACGAA 180
DB |||||||
QY 125 GCCCAGGATTCGACTCAGCGCTTCCCTCAGGCGGCTCTCTCTCTACCGAATACGAA 184
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QY 181 CGCTTCTTCGCTACTGCTGCTCAACTGGAAGGAGAGACTACCTGCGCTTCGCTGCA 240
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QY 185 CGCTTCTTCGCTACTGCTGCTCAACTGGAAGGAGAGACTACCTGCGCTTCGCTGCA 244
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QY 241 ACCCAGGCTGCGGATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
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Site 2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

RESULT 3
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DEFINITION AGENCOURT_6560348 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5741926
5', mRNA sequence.
ACCESSION BM563837
VERSION BM563837.1 GI:18811108
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1093)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

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QY 541 TTCCAGCCCTGCTGAGAGGCTCAGCAACAGCTGGAAGTCTCTACATCTCTCTG 600
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DB |||||||
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QY 605 TCCCTGGAGGCGCAGGAGCAAGCGCCAGAGCAACAGCTGGAAGTCTCTACATCTCTG 664
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QY 661 CAGGAGCGGACACACAGAACACCAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
DB |||||||
QY 665 CAGGAGCGGACACACAGAACACCAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 724
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QY 721 GAACAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
DB |||||||
QY 725 GAACAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 784
DB |||||||
QY 781 GTGTCTCAGCTGCAGACAGACTCAGA 806
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directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

```

(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

ORIGIN	Query Match	Best Local Similarity	Score	DB 4	Length	1093	Mismatches	1	Indels	0	Gaps	0
QY	19	CCACGGGACGGCGGATCTTCTCCGCCATGAGGAGCCAGCGCTGGCTTCCCTCC	78									
Db	21	CCACGGGACGGCGGATCTTCTCCGCCATGAGGAGCCAGCGCTGGCTTCCCTCC	80									
QY	79	TCACTCTGGAAGTGTCTCTCTCCCTCTGCACTCCCGCAGCCAGGATTCGACTCAG	138									
Db	81	TCACTCTGGAAGTGTCTCTCTCCCTCTGCACTCCCGCAGCCAGGATTCGACTCAG	140									
QY	139	GCCCCCACTCAGCAGCCCTCTCTCTACCGAATACGAAGCTTCTTCGACTGCTG	198									
Db	141	GCCTCCACTCCAGCAGCCCTCTCTCTACCGAATACGAAGCTTCTTCGCACTGCTG	200									
QY	199	ACTCCAACTTGAAGGACAGACTTCTGCGTCTCGTGCAACCCAGCGCTGCCGAAT	258									
Db	201	ACTCCAACTTGAAGGACAGACTTCTGCGTCTCGTGCAACCCAGCGCTGCCGAAT	260									
QY	259	CCCACTCTGTCAGCTGGAACCAATATGAAACCAACCGCTTAGTGCCCGATGCTGTC	318									
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QY	379	TGCTCCAACTTCCCTATGCTCTCTGTTGAGTCTTCTGCGAGTCTCTATTCTC	438									
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QY	439	TCACCTAACACTTCAAGGATAGAGCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAG	498									
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QY	499	TCCCCATCTCACCCACTTTCAGAGTACAGAGGAGGAGGAGGAGGAGGAGGAGG	558									
Db	501	TCCCCATCTCACCCACTTTCAGAGTACAGAGGAGGAGGAGGAGGAGGAGGAGG	560									
QY	559	AGGCTCAGCAACACGCTGGAAGAGCTCTTCAATCTCTCTGCTGCGAGGAGGAGG	618									
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QY	619	CAAGCGCAGACCAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	678									
Db	621	CAAGCGCAGACCAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	680									
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QY	739	AAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	798									
Db	741	AAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	800									
QY	799	GACTCAGAGCCCAAGTTTCACTCTG	823									
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5', mRNA sequence.
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BM554354
VERSION
BM554354.1 GI:18793882
KEYWORDS
EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1037)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cdna Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12760 row: 1 column: 03
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/note="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

ORIGIN

Query Match	Best Local Similarity	Score	DB 4	Length	1037	Mismatches	0	Indels	0	Gaps	0
QY	39	TTCTCCGGCCATGAGGAGCCAGCGCTGGCTTCTCCCTCACTCTCGAGGTGCTGCT	98								
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QY	99	CCTGCTCTGGCACTGCGCAGCCAGGATTCGACTCAGGCCCCCACTCCAGGAGGAGG	158								
Db	86	CCTGCTCTGGCACTGCGCAGCCAGGATTCGACTCAGGCCCCCACTCCAGGAGGAGG	145								
QY	159	TCTCTCTCTACCGAATACGAAACGCTTCTTCGCACTGCTGCTCCAACTCGGAGGAGG	218								
Db	146	TCTCTCTCTACCGAATACGAAACGCTTCTTCGCACTGCTGCTCCAACTCGGAGGAGG	205								
QY	219	GACTACTTGGCGTCTCCGTCGCAACCCAGCGCTGCGGAAATCCCACTCGTCAGGTGGA	278								
Db	206	GACTACTTGGCGTCTCCGTCGCAACCCAGCGCTGCGGAAATCCCACTCGTCAGGTGGA	265								
QY	279	CCAATATGAAAACCAACCGGCTTAGTGCCGATGCTGCTGCTCCAACTCCCTTATGC	338								
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QY	339	CTCCTGTTTGGTCTTTCTGCGGAGTTCCTACTACCGTTCCTCCAACTCGTCTACTA	398								
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QY	399	TGCCAAGAGAGTCTGTGTTCCAGCCAGTCTCTATTCTCTCACCTAACACTCTCAAGGA	458								
Db	386	TGCCAAGAGAGTCTGTGTTCCAGCCAGTCTCTATTCTCTCACCTAACACTCTCAAGGA	445								
QY	459	GATAGAGCTTCAGCTGAAGTCTCACCCAGAGTACCTCCCTCCATCTCACCCCATCTT	518								


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Db 81 CACTCTGAAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 140
Qy 140 CCCCCACTCCAGGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 199
Db 141 CTTCCACTCCAGGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 200
Qy 200 CTTCCAACTGGAAGGAGAGACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 259
Db 201 CTTCCAACTGGAAGGAGAGACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 260
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Qy 440 CACCTTAACACTCTCAAGGAGATAGACTTCACTCAAGTCTCACCACCAAGTACCT 499
Db 441 CACCTTAACACTCTCAAGGAGATAGACTTCACTCAAGTCTCACCACCAAGTACCT 500
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Qy 560 GGTCTAGCAACAACTGGAAGAGCTCTCAATCTCTCTCTCTCTCTCTCTCTCTCT 619
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Db 741 AGCAGGAAGAAGG 753
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5', mRNA sequence.
BM554519
VERSION NIH-MGC http://mgi.nci.nih.gov/
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM12760 row: p column: 01
High quality sequence stop: 673.

FEATURES

source

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/clone_lib="NIH_MGC_119"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 35.8%; Score 678; DB 4; Length 1012;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 65 CTCCTGAAGTGTCT 124
Qy 142 CCCACTCCAGGAGCGCT 201
Db 125 TCCACTCCAGGAGCGCT 184
Qy 202 CCAACTGGAAGGAGAGACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 261
Db 185 CCAACTGGAAGGAGAGACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 244
Qy 262 ACACCTGTCAGCTGGACCAATATGAAACACAGCGCTTAGTGGCCGATGGTGTCTGC 321
Db 245 ACACCTGTCAGCTGGACCAATATGAAACACAGCGCTTAGTGGCCGATGGTGTCTGC 304
Qy 322 TCCAACT 381
Db 305 TCCAACT 364
Qy 382 TCCAACT 441
Db 365 TCCAACT 424
Qy 442 CTTAACTCTCTCAAGGAGATAGAGCTTCAGCTGAAGTCTCACCCACCAAGTACCTCC 501
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Qy 502 CTTAACTCTCTCAAGGAGATAGAGCTTCAGCTGAAGTCTCACCCACCAAGTACCTCC 561
Db 485 CTTAACTCTCTCAAGGAGATAGAGCTTCAGCTGAAGTCTCACCCACCAAGTACCTCC 544
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Site 2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dr primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

ORIGIN
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 61 TGATGAGAACTCTACTGGAGAAACCAAAACCTTGCAGCTTCTGCAGCTGCCCAAC 120
QY 1014 AGAGGCTTGTGCTGTGCTATTCGATCTGGAGAAATACCTGATCATATACCCCCAC 1073
DB 121 AGAGGCTTGTGCTGTGCTATTCGATCTGGAGAAATACCTGATCATATACCCCCAC 180
QY 1074 AGCCAGGCTGGAAGTACATGAGGAGGAGATCTTGTGTTTCGGGAAGTCGGTCTGTGA 1133
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VERSION BI520181.1 GI:15344973
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 827)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11405 row: j column: 07
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Site 2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dr primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."
ORIGIN
Query Match 35.4%; Score 670; DB 4; Length 827;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 670; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L14M11416 row: n column: 17
 High quality sequence stop: 684.
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 Site 2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library."

FEATURES

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 Site 2: EcoRV (destroyed); RNA source normal medulla from
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 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library."

Query Match

35.2%; Score 667; DB 4; Length 718;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1228 CAACATGCGACACCTCCCAAGACTCCCTTTGTGACCCCTTGTCTTCCAGAGC 1287
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 Db 121 TAGGTGGGCTCCCAATGAGTCTTGTGTGTCGCCGGCTTCCAGAGGCTGGAATTG 180
 QY 1408 GTCCAGTCTCTGGGTGGCTCCAGACTGAGTCTTGTGTGTCGCCGGCTTCCAGAGGCTGGAATTG 1467
 Db 181 GTCCAGTCTCTGGGTGGCTCCAGACTGAGTCTTGTGTGTCGCCGGCTTCCAGAGGCTGGAATTG 240
 QY 1468 ACCAAGATTTGTGACACAGACTATATCCAGTACCCAACTACTGTTCTTCAAAAGCCAG 1527
 Db 241 ACCAAGATTTGTGACACAGACTATATCCAGTACCCAACTACTGTTCTTCAAAAGCCAG 300
 QY 1528 CAGTGTCTGATGAGAAACCCGCAATCCGAAAGTGTCCGCAATGAGTGTCTGCAAGATGAG 1587
 Db 301 CAGTGTCTGATGAGAAACCCGCAATCCGAAAGTGTCCGCAATGAGTGTCTGCAAGATGAG 360
 QY 1588 ACTTACAGTGGCTGAGCCCTGGCAAAAGTGAAGAGTGTGTCGCCGGCTTCCAGAGGCTGGAATTG 1647
 Db 361 ACTTACAGTGGCTGAGCCCTGGCAAAAGTGAAGAGTGTGTCGCCGGCTTCCAGAGGCTGGAATTG 420
 QY 1648 TTGACGACCTTGAATCTAGGCTGAGTGTGAGTGTGTCGCCGGCTTCCAGAGGCTGGAATTG 1707
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 QY 1708 GCCCAACCTGCCACGTTCTTATTTGTGACCCCTTGTGTCGCCGGCTTCCAGAGGCTGGAATTG 1767
 Db 481 GCCCAACCTGCCACGTTCTTATTTGTGACCCCTTGTGTCGCCGGCTTCCAGAGGCTGGAATTG 540
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 Db 661 AAAAAA 667

RESULT 13

BI520377
 LOCUS
 DEFINITION
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 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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FEATURES
source

ORIGIN
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 716; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 61 GCCGTGGCTTCTTCCCTCACTCTCTGAAGTGTCTCTCTGCTGTGGCCTTCCGCA 120
DB 86 GCCGTGGCTTCTTCCCTCACTCTCTGAAGTGTCTCTCTGCTGTGGCCTTCCGCA 145
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DB 626 TCCCTGGGAGGCCAGGAGCAAGCGCCAGAGCAAGCAGGAGCAAGGAGTGGAGCACAGG 685

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mRNA sequence.
ACCESSION
BI520136
VERSION
BI520136.1 GI:15344928
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 891)
NIH-MGC <http://mgc.nci.nih.gov/>
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM11405 row: e column: 20
High quality sequence stop: 843.
Location/Qualifiers
1. .891
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/clone="IMAGE:5163259"
/tissue_type="medulla"
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/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

FEATURES
source

ORIGIN
Query Match 35.1%; Score 665; DB 4; Length 891;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 715; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 195 CGCTTCTTCGCACTGTCTGCTCCAACTCGAAGGACAGACTACCTGCGCTCTCGTGCA 244

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2005, 14:11:37 ; Search time 7500 Seconds

(without alignments)
9617.572 Million cell updates/sec

Title: US-09-559-013E-23

Perfect score: 1895

Sequence: 1 gtagagcggtgtgtcc.....tgtagatctcaaaaaaaaaa 1895

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hcc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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2	942.4	49.7	1026	4	BM553910	BM553910 AGENCOURT
3	936.2	49.4	1076	4	BM564020	BM564020 AGENCOURT
4	928.8	49.0	1074	4	BM563920	BM563920 AGENCOURT
5	925.6	48.8	1023	4	BM554310	BM554310 AGENCOURT
6	909	48.0	1093	4	BM563837	BM563837 AGENCOURT
7	888.8	46.9	1122	4	BM553334	BM553334 AGENCOURT
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10	828	43.7	891	4	BM520136	BM520136 603071275
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12	799.2	42.2	825	4	BM825274	BM825274 603071974
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14	788	41.6	854	4	BM826371	BM826371 603076231
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16	779.4	41.1	847	4	BM829134	BM829134 603079220
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22	752	39.7	843	4	BM831575	BM831575 603074605
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28	723.4	38.2	737	4	BI829870	BI829870 603079974
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30	722	38.1	769	4	BI520377	BI520377 603071855
31	718.2	37.9	753	4	BI829635	BI829635 603079374
32	717.2	37.8	762	4	BI463234	BI463234 603073124
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ALIGNMENTS

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VERSION BM554354.1 GI:18793882
KEYWORDS EST.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1037)
AUTHORS NIH-MGC <http://mgc.nhl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12760 row: 1 column: 03
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FEATURES

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ORIGIN

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Matches 1007; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

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DB 80 GCTGCTCTGCTCTGCGACTGCGGAGCCAGGAGGATTCAGTCAAGGCCCCCACTCAGG 139

QY 153 CAGCCCTCTCTCTACCGAATACGAAACGCTTCTCGCACTGCTGACTCAACCTGGAA 212
DB 140 CAGCCCTCTCTCTACCGAATACGAAACGCTTCTCGCACTGCTGACTCAACCTGGAA 199

QY 213 GGCAGAGACTACTGCGCTCTCGGTGCAACCCAGGCTGCCGAATCCCACTCTGTC 272
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DB 440 CAAGGAGATGAGACTTCACTGAGTCTCAACCCAGGATGACCTCCCGCATCTCACC 499

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  BM553910.1 GI:18793058
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  SOURCE
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 1026)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-roman@nih.gov
  Tissue Procurement: Life Technologies, Inc.
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLNL12760 row: a column: 11
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  Site 2: EcoRV (destroyed); RNA source normal medulla from
  anonymous male age 27. Library is oligo-dT primed and
  directionally cloned (EcoRV site is destroyed upon
  cloning). Average insert size 1.3 kb, insert size range
  0.9-3 kb. Library is normalized and enriched for
  full-length clones and was constructed by C. Gruber
  (Invitrogen). Research Genetics tracking code 013. Note:
  this is a NIH_MGC Library."
ORIGIN
Query Match      49.7%; Score 942.4; DB 4; Length 1026;
Best Local Similarity 97.0%; Pred. No. 1.6e-224;
Matches 992; Conservative 0; Mismatches 27; Indels 4; Gaps 3;

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QY 121 GCCCAGGATTGACTCAGGCGCCCACTCCAGGCGCCCTCTCTCTCTACCGAATACGAA 180
DB 125 GCCCAGGATTGACTCAGGCGCCCACTCCAGGCGCCCTCTCTCTCTACCGAATACGAA 184

QY 181 GCCTTCTTCCGACTGCTCTCAACCTGGAAGGAGAGACTACCTGCGCTTCCGTCGA 240
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Db 305 GTGCCGATGGTGTCTCTCTCCAACTCCCTTATGCTCCTCGTTTGAGTCTTTCTGTC 364
 QY 361 CAGTTCACTCACTACCGTGTCTCCACAGCTCTACTATGCGCAAGAGAGTCTGTGTTCC 420
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 REFERENCE 1 (bases 1 to 1076)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAM12759 row: i column: 17
 High quality sequence stop: 758.
 Location/Qualifiers
 1. 1076
 /organism="Homo sapiens"
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 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 49.4%; Score 936.2; DB 4; Length 1076;
 Best Local Similarity 99.0%; Pred. No. 5,7e-223;
 Matches 963; Conservative 0; Mismatches 8; Indels 2; Gaps 2;
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 Db 21 CGGGACGCGGGCGGATCTTCTCGGCAATGAGGAAGCCAGCGCTGGCTTCTTCCCTCA 80
 QY 82 CTCCTGAAGGTCTGCTCTCTGCTCTGCACTGCGCAGCCAGGATTGCACTCAGGCC 141
 Db 81 CTCCTGAAGGTCTGCTCTCTGCTCTGCACTGCGCAGCCAGGATTGCACTCAGGCC 140
 QY 142 CCCACTCCAGGCGAGCCCTCTCTCTACCGAATACGAAGCTTCTTCGCACTGCTGACT 201
 Db 141 TCCACTCCAGGCGAGCCCTCTCTCTACCGAATACGAAGCTTCTTCGCACTGCTGACT 200
 QY 202 CCACCTGGAAGCGAGAGACTACTCTCGCTCTCCGTCGCAACCCAGCGCTGCCGAATCCC 261
 Db 201 CCACCTGGAAGCGAGAGACTACTCTCGCTCTCCGTCGCAACCCAGCGCTGCCGAATCCC 260
 QY 262 ACACCTGCTCCAGCTGGACCAATATGAAACCAACGCGCTTAGTGCCTGATGCTGTGC 321
 Db 261 ACACCTGCTCCAGCTGGACCAATATGAAACCAACGCGCTTAGTGCCTGATGCTGTGC 320
 QY 322 TCCAACTCTCCCTTATGCTCTGCTGCTTGTGAGTCTTTCTGCGAGTTCACTACCGTTGC 381
 Db 321 TCCAACTCTCCCTTATGCTCTGCTGCTTGTGAGTCTTTCTGCGAGTTCACTACCGTTGC 380
 QY 382 TCCAACTCTCTACTTATGCTCCAGAGAGTCTGTGTTCCAGCGAGCTCTTATTTCTCA 441
 Db 381 TCCAACTCTCTACTTATGCTCCAGAGAGTCTGTGTTCCAGCGAGCTCTTATTTCTCA 440
 QY 442 CTTAACTCTCTCAAGGAGATAGAAGCTTCAGCTGAAGTCTCAGCCACCGAGTACCTCC 501
 Db 441 CTTAACTCTCTCAAGGAGATAGAAGCTTCAGCTGAAGTCTCAGCCACCGAGTACCTCC 500
 QY 502 CCCATCTACCCCACTTCACTGACAGAACGCGAGACCTTCCAGCCCTGGCTGAGAGG 561
 Db 501 CCCATCTACCCCACTTCACTGACAGAACGCGAGACCTTCCAGCCCTGGCTGAGAGG 560
 QY 562 CTCACCAACAGTGGAGAGCTCTTCAATCTCTGCTGCTGGAGGCGCAGGAGCA 621
 Db 561 CTCACCAACAGTGGAGAGCTCTTCAATCTCTGCTGCTGGAGGCGCAGGAGCA 620
 QY 622 GCGCCAGAGCAACAGCAGGAGCAAGGAGTGGAGCAGCAGGAGCGGAGCCGACAAAGAAC 681
 Db 621 GCGCCAGAGCAACAGCAGGAGCAAGGAGTGGAGCAGCAGGAGCGGAGCCGACAAAGAAC 680


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Db      1033 ATTCCACGGGAAAAAAACCTGAATATTAACCCCA 1068
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RESULT 5
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5', mRNA sequence.
ACCESSION
BM554310
VERSION
BM554310.1 GI:18793801
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1023)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12760 row: k column: 04
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/clone_lib="NIH_MGC_119"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."
ORIGIN
Query Match 48.8%; Score 925.6; DB 4; Length 1023;
Best Local Similarity 97.4%; Pred. No. 2.5e-220;
Matches 982; Conservative 0; Mismatches 21; Indels 5; Gaps 4;
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DB 16 GGGATCAGGGACGGGGGGGATCTTCTCGGCCATGAGGAAGCCAGCGCTGGCTTCT 75
QY 75 TCCTTCACCTCCCTGAGGTGCTGCTCTGCTCTGCGACCTGCGGACGCCAGGATTCGAC 134
DB 76 TCCTTCACCTCCCTGAGGTGCTGCTCTGCTCTGCGACCTGCGGACGCCAGGATTCGAC 135
QY 135 TCAGGCCCCCACTCCAGGAGCGCCCTCTCTCTCTACCGAATACGAACGCTTCTTCGCAT 194
DB 136 TCAGGCCCCCACTCCAGGAGCGCCCTCTCTCTCTACCGAATACGAACGCTTCTTCGCAT 195
QY 195 GCTGATCTCAACCTCGAAGCGAGAGACTACTGCGGTCTTCGTGCAACCCAGCGGTGCGG 254
DB 196 GCTGATCTCAACCTCGAAGCGAGAGACTACTGCGGTCTTCGTGCAACCCAGCGGTGCGG 255
QY 255 GAATCCCACTCCCTGAGGTGCTGCTCTGCTCTGCGACCTGCGGACGCCAGGATTCGAC 314
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Db      256 GAATCCCACTCCCTGAGGTGCTGCTCTGCGACCTGCGGACGCCAGGATTCGAC 315
QY 315 TGTCTGCTCCAAACCTCCCTTATGCTCTCTGGTTTGAAGTCTTTCTGCGAGTTCACTACTA 374
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QY 375 CGTTTGTCTCCAAACCTCCCTTATGCTCTCTGGTTTGAAGTCTTTCTGCGAGTTCTCTAT 434
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QY 435 TCTCTCACCTTAACACTCTCAAGGAGATAGAAGCTTCAGCTGTAAGTCTCACCCACCGAT 494
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DB 496 GACCTCCCCCTCTCAACCTCTCAAGGAGATAGAAGCTTCAGCTGTAAGTCTCACCCACCGAT 555
QY 555 TGAGAGGCTCAGCAACAGTGAAGAGTCTCTTACAACTCTCTCTGCTCCCTGGGAGGCCA 614
DB 556 TGAGAGGCTCAGCAACAGTGAAGAGTCTCTTACAACTCTCTCTGCTCCCTGGGAGGCCA 615
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DB 736 GGGAAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 795
QY 794 AGACAGACTCAGAGCCCAAGTTTCACTCTGAATCTCTATCTTCTTAACCTCTCTCTTTG 853
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DB 916 CTCATTGATCAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 975
QY 970 TGGAGAAACCAAAACCTGCGAGCTTCTCTGAGCTGCTCCCAACACACAGAG 1017
DB 976 TGGAGAAACCAAAACCTGCGAGCTTCTGAGCTGCTCCCAACACAAAG 1023
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ACCESSION
BM563837
VERSION
BM563837.1 GI:18811108
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1093)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLAM12759 row: d column: 23
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High quality sequence stop: 724.

FEATURES

source

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/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 48.0%; Score 909; DB 4; Length 1093;
Best Local Similarity 94.2%; Pred. No. 3.7e-216;
Matches 1011; Conservative 0; Mismatches 50; Indels 12; Gaps 6;

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DB 81 TCATCTCTGAAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 140
QY 139 GCGCCCACTCCAGCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 198
DB 141 GCCTCCACTCCAGCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 200
QY 199 ACTCCAACTCCGAGGACAGACTACTCTGCGCTCTGCGCTCTGCGCTCTGCG 258
DB 201 ACTCCAACTCCGAGGACAGACTACTCTGCGCTCTGCGCTCTGCGCTCTGCG 260
QY 259 CCCACACTCTCAGCTGAGCCAAATGAAACCCAGCGCTTAGTGCCTGATGCT 318
DB 261 CCCACACTCTCAGCTGAGCCAAATGAAACCCAGCGCTTAGTGCCTGATGCT 320
QY 319 TGCTCCAACTCTCTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 378
DB 321 TGCTCCAACTCTCTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 380
QY 379 TGCTCCAACTCTCTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 438
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DB 861 CCGGGTACGAGAGTAGAGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 920
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BM553134 1122 bp mRNA linear EST 20-FEB-2002
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BM553134
BM553134.1 GI:18791598
EST.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1122)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12761 row: k column: 05
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FEATURES

source

Location/Qualifiers
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(Invitrogen). Research Genetics tracking code 013. Note: this is a NIH MGC Library."

ORIGIN

[illegible]

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Db	1044	ACAAAGGCCCTTTGCTGGGGGTTGGGCAATTTCATCGGGAAGAAAACCTGCATATATA	1103
Qy	1067	CCCCACAGCCAAAGGC	1082
Db	1104	CCCCACAGCACAGGC	1119
RESULT 8			
LOCUS	BM554519	1012 bp	linear
DEFINITION	AGENCOURT_6546640 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742576	5', mRNA sequence.	EST 20-FEB-2002
ACCESSION	BM554519		
VERSION	BM554519.1	GI:18794182	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1012)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabs@email.nih.gov		
	Tissue Procurement: Life Technologies, Inc.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov		
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FEATURES			
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	/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 Kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."		
ORIGIN			
Query Match	45.5%	Score 861.8;	DB 4; Length 1012;
Best Local Similarity	97.0%;	Pred. No. 2.3e-204;	
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Db	3	CCCGGACCGCGCGGATCTTCTCCGGCATGAGGACCGCGCTGGCTTCCCTCCCT	62
Qy	80	CATCTCTGAAGTGTGCTCTCGCTCTGGACCTGCGCAGCCAGGATTCGACTCAGG	139
Db	63	CATCTCTGAAGTGTGCTCTCGCTCTGGACCTGCGCAGCCAGGATTCGACTCAGG	122
Qy	140	CCCCCACTCCAGGACGCCCTCTCTCTCTACCGAATACGAACGCTCTTCGCACTGCTGA	199

Email: cgapbs@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11407 row: f column: 05
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 Site 2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library."

ORIGIN

Query Match 43.4%; Score 823.2; DB 4; Length 991;
 Best Local Similarity 97.8%; Pred. No. 1.1e-194;
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QY	82	CTCTGAAGTGCTGCTCTGCGCTCTGCGACCTGCGCGAGCGCGGATTCGACTAGGC	141
Db	61	CTCTGAAGTGCTGCTCTGCGCTCTGCGACCTGCGCGAGCGCGGATTCGACTAGGC	120
QY	142	CCCACTCCAGGCGGCTCTCTCTACGGAATACGAACGGTTCTTTCGCTGAC	200
Db	121	TCCACTCCAGGCGGCTCTCTCTACGGAATACGAACGGTTCTTTCGCTGAC	180
QY	201	TCCAACTGGAAGCGAGACTACCTGCGCTCTCGTGCAACCCAGCGGTCGGGATCC	260
Db	181	TCCAACTGGAAGCGAGACTACCTGCGCTCTCGTGCAACCCAGCGGTCGGGATCC	240
QY	261	CACACTGCTCAGCTGGAACAATATGAAACCAACCGCTTAGTGCCGATGCTGCTG	320
Db	241	CACACTGCTCAGCTGGAACAATATGAAACCAACCGCTTAGTGCCGATGCTGCTG	300
QY	321	CTCCAACTCCCTTATGCTCTGCTGTTTTCAGTCTTTCGCGAGTTCACCTACCGTTG	380
Db	301	CTCCAACTCCCTTATGCTCTGCTGTTTTCAGTCTTTCGCGAGTTCACCTACCGTTG	360
QY	381	CTCCAACTCCCTTATGCTCTGCTGTTTTCAGTCTTTCGCGAGTTCACCTACCGTTG	440
Db	361	CTCCAACTCCCTTATGCTCTGCTGTTTTCAGTCTTTCGCGAGTTCACCTACCGTTG	420
QY	441	ACCTACACTCTCAGGAGATAGAGCTTCAGCTGAGTCTCACCACAGATGACCTC	500
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QY	501	CCCATCTCACCCTTACAGTACAGAGCGGCGAGACCTTCCAGCGCTGCGCTGAG	560
Db	481	CCCATCTCACCCTTACAGTACAGAGCGGCGAGACCTTCCAGCGCTGCGCTGAG	540
QY	561	GCTCAGCAACAGTGGAGAGCTCCTCAATTCCTTGTCTCTGGGAGGCGGAGCA	620
Db	541	GCTCAGCAACAGTGGAGAGCTCCTCAATTCCTTGTCTCTGGGAGGCGGAGCA	600

QY	621	AGCCCCAGAGCACAAGCAGGAGCAAGGAGTGGAGCAGGAGGAGCGGACACAAAGAA	680
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Db	781	ACTCAGAGCCCAAGTTTCACTCTGAATCTCTA-TCTTCTAACCCCTTCTCTTTT--GCTC	840
QY	857	CCCGGTACGAGAGTACTCTCTCTATGATATGAGAAAC-TCCAGGAGTCA-T	914
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QY	915	TCGATCAGCCCGAGGAAAT	932
Db	901	TCGATCAGCCCGAGGAAAT	918

RESULT 12

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 BI825274.1 GI:15936824
 EST.
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11407 row: c column: 19
 High quality sequence stop: 825.
 Location/Qualifiers
 1. .825
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 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library."

FEATURES
source

ORIGIN

Query Match 42.2%; Score 799.2; DB 4; Length 825;
Best Local Similarity 98.8%; Pred. No. 1.1e-198;
Matches 815; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 22 CGGACCGCGCGGATCTTCTCGGCCATGAGGAAGCCAGCGCTGCTTCCCTCA 81
DB 1 CGGACCGCGCGGATCTTCTCGGCCATGAGGAAGCCAGCGCTGCTTCCCTCA 60

QY 82 CTCTGAAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 141
DB 61 CTCTGAAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

QY 142 CCACCTCCAGCGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 201
DB 121 TCCACTCCGAGCGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180

QY 202 CCAACCTGGAAGCAGAGACTACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 260
DB 181 CCAACCTGGAAGCAGAGACTACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

QY 261 CACACTGCTCAGCTGAGCAATATGAACCAACCGCTTGTAGTCCCGATGCTGCTG 320
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QY 321 CTCACACTCTCTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 380
DB 301 CTCACACTCTCTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360

QY 381 CTCACACTCTCTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 440
DB 361 CTCACACTCTCTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420

QY 441 ACCTACACTCTCAGGAGATAGAGCTTCACTGAGTCTCACTGAGTCTCACTGAGT 500
DB 421 ACCTACACTCTCAGGAGATAGAGCTTCACTGAGTCTCACTGAGTCTCACTGAGT 480

QY 501 CCCCATCTCACCCACTTTCAGTGCAGAGACGAGAGCTTCCAGCCCTGGCTGAGAG 560
DB 481 CCCCATCTCACCCACTTTCAGTGCAGAGACGAGAGCTTCCAGCCCTGGCTGAGAG 540

QY 561 GCTCAGCAACAGTGAAGAGTCTCTCAATCTCTCTCTCTCTCTCTCTCTCTCTCT 620
DB 541 GCTCAGCAACAGTGAAGAGTCTCTCAATCTCTCTCTCTCTCTCTCTCTCTCTCT 600

QY 621 AGCGCAGAGCAACGAGAGCAAGAGTGGAGCAGCAGCAGGAGCCGACAGAGCA 680
DB 601 AGCGCAGAGCAACGAGAGCAAGAGTGGAGCAGCAGCAGGAGCCGACAGAGCA 660

QY 681 CAAGCAGGAGAGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 740
DB 661 CAAGCAGGAGAGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720

QY 741 GCAGGAG 800
DB 721 GCAGGAG 780

QY 801 CTGAGAGCCCAAGTTTCACTCTGAAATCTTAATCTTCTTAACCCCTTC 845
DB 781 CTGAGAGCCCAAGTTTCACTCTGAAATCTTAATCTTCTTAACCCCTTC 825

RESULT 13

BI828365
LOCUS 603078309F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5170058 5',
DEFINITION mRNA sequence.
ACCESSION BI828365
VERSION BI828365.1 GI:15939915
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 823)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-x@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNL1423 row: a column: 03
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FEATURES

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Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match 41.9%; Score 793.6; DB 4; Length 823;
Best Local Similarity 99.3%; Pred. No. 2.6e-187;
Matches 818; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 36 ATCTTCTCGGCGCATGAGGAAGCCAGCGCTGCTTCTTCTCTCTCTCTCTCTCTCT 95
DB 1 ATCTTCTCGGCGCATGAGGAAGCCAGCGCTGCTTCTTCTCTCTCTCTCTCTCTCT 60

QY 96 GCTCTGCTCTGCGCAGCTGCGCAGCAGCAGGATTCGACTCAGGCCCCCACTCAGGAG 155
DB 61 GCTCTGCTCTGCGCAGCTGCGCAGCAGCAGGATTCGACTCAGGCCCCCACTCAGGAG 120

QY 156 CCTCTCTCTCTTACCGAATAGGAAGCTTCTTTCGCACTGCTGCTGCTGCTGCTGCT 215
DB 121 CCTCTCTCTCTTACCGAATAGGAAGCTTCTTTCGCACTGCTGCTGCTGCTGCTGCT 180

QY 216 AGAGACTACTGCTGCTCTCTCGTGCAACCCAGCGCTGCGGGAATCCCACTCTCGTCCAGCT 275
DB 181 AGAGACTACTGCTGCTCTCGTGCAACCCAGCGCTGCGGGAATCCCACTCTCGTCCAGCT 240

QY 276 GGACCAATATGAAACACAGGCTTAGTGGCGAGTGTGTGTGTGTGTGTGTGTGTGT 335
DB 241 GGACCAATATGAAACACAGGCTTAGTGGCGAGTGTGTGTGTGTGTGTGTGTGTGT 300

QY 336 TGCCTCTCTGTTGAGTCTTCTGCGAGTTCCTACTACCGTTGCTCCCAACCACTCTA 395
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QY 396 CTATGCCAAGAGAGTCTCTGTGTTTCCAGCGAGTCTCTATTCTCTCACTTAACTCTCAA 455
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QY 456 GGAGATAGAGCTTTCAGTGAAGTCTCAACCCAGCAGTGAAGTCTCCCACTCTCAACCCCA 515
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Db 541 GGAAGAGTCTTACAACTCTTCTCTTCTCTTCTCTTCTCTTCTCTTCTCTTCTCTTCT 600

Qy 636 GCAGGAGCAGAGGAGTGGAGCAGCAGCAGGAGCCGACACAAACACACAGCAGGAGGG 695

Db 601 GCAGGAGCAGAGGAGTGGAGCAGCAGCAGGAGCCGACACAAACACACAGCAGGAGGG 660

Qy 696 GCAGAAACAGAGAGCAG 755

Db 661 GCAGAAACAGAGAGCAG 720

Qy 756 GGGGAGTAAAGAGGAGCAGGAGGAGTGTCTCAGCTGACAGCAGCAGCAGCAGCAGCAG 815

Db 721 GGGGAGTAAAGAGGAGCAGGAGGAGTGTCTCAGCTGACAGCAGCAGCAGCAGCAGCAG 779

Qy 816 TCACCTGAACTCTATCTTCT-AACCCCTTCTCTCTTTTGTCTCC 858

Db 780 TCACCTGAACTCTATCTCTTAAACCCCTTCTCTTTGTCTCC 823

RESULT 14

BI826371

LOCUS 603076231F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5168070 5', mRNA sequence.

DEFINITION

ACCESSION BI826371

VERSION BI826371.1 GI:15937921

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Plate: L1AM11417 Row: n column: 07
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Location/Qualifiers
1. 854
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/clone_lib="NIH_MGC_119"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

FEATURES
source

ORIGIN

Query Match 41.6%; Score 788; DB 4; Length 854;
Best Local Similarity 98.8%; Pred. No. 6.7e-186;
Matches 846; Conservative 0; Mismatches 5; Indels 5; Gaps 5;

Qy 17 GTCCAGGACGCGGCGGATCTTCTCCGGCCATGAGGAAGCCAGCGCTGGCTTCCTTC 76

Db 1 GTCCAGGACGCGGCGGATCTTCTCCGGCCATGAGGAAGCCAGCGCTGGCTTCCTTC 60

Qy 77 CTTCACTCTCTGAGGTGTCT 136

Db 61 CTTCACTCTCTGAGGTGTCT 120

Qy 137 AGGCCCCCACTCCAGCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 196

Db 121 AGGCTCTCACTCCAGCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180

Qy 197 TGACTCCAACTCTGAGGAGCAGAGCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 256

Db 181 TGACTCCAACTCTGAGGAGCAGAGCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240

Qy 257 ATCCACACACTCTGAGGAGCAGAGCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 316

Db 241 ATCCACACACTCTGAGGAGCAGAGCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300

Qy 317 TCTGCTCCAACT 376

Db 301 TCTGCTCCAACT 360

Qy 377 GTTGTCTCAACCACT 436

Db 361 GTTGTCTCAACCACT 420

Qy 437 TCTCACTTAACACTCTCAAGGAGATAGAACTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 496

Db 421 TCTCACTTAACACTCTCAAGGAGATAGAACTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 480

Qy 497 CTTCCCTCCATCTCACTCTCAAGGAGATAGAACTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 556

Db 481 CTTCCCTCCATCTCACTCTCAAGGAGATAGAACTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 540

Qy 557 AGAGGCTCAGCAACAAGTGGAGAGCTCTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 615

Db 541 AGAGGCTCAGCAACAAGTGGAGAGCTCTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 600

Qy 616 GAGCAAGCCGAGAGCAGCAGGAGCAGGAGTGGAGCAGCAGGAGCAGGAGCAGGAGCAGGAG 675

Db 601 GAGCAAGCCGAGAGCAGCAGGAGCAGGAGTGGAGCAGCAGGAGCAGGAGCAGGAGCAGGAG 660

Qy 676 GAAACAGCAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 735

Db 661 GAAACAGCAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720

Qy 736 GGAAGACA-GGAAGAGCAGAGGG-GACTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 793

Db 721 GGAAGACA-GGAAGAGCAGAGGG-GACTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780

Qy 794 AGACAGACTCAGAGCCCAAGTTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTTTG 853

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Qy 854 CTCCCCGGGTACGAGA 869

Db 839 CTCCCCGGGTACGAGA 854

RESULT 15

BI520181

LOCUS 603071429F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:516366 5', mRNA sequence.

DEFINITION

ACCESSION BI520181

VERSION BI520181.1 GI:15344973

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 827)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM11405 row: j column: 07
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 /note="Organ: brain; Vector: pCMV-SPORT6; Site:1: NotI;
 Site:2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library."

FEATURES

source

ORIGIN

Query Match 41.3%; Score 782.8; DB 4; Length 827;
 Best Local Similarity 98.3%; Pred. No. 1.3e-184;
 Matches 812; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

QY 1033 TGCTATTCGATCGTGAGAAATACCTGCATCATACCAACCCACAGCCCAAGCCCTGGAGTAC 1092
 DB 1 TGCTATTCGATCGTGAGAAATACCTGCATCATACCAACCCACAGCCCAAGCCCTGGAGTAC 60

QY 1093 ATGGAGGAGAGATCCTTGGTTTCGGGAAGTCGGTCTGTGACAGCCTTGGGCGGACAC 1152
 DB 61 ATGGAGGAGAGATCCTTGGTTTCGGGAAGTCGGTCTGTGACAGCCTTGGGCGGACAC 120

QY 1153 ATGTCTACCTGTGCCCTCTGTGACTTCTGCTCTTGAAGCTGGAGTGGCCACTCAGAG 1212
 DB 121 ATGTCTACCTGTGCCCTCTGTGACTTCTGCTCTTGAAGCTGGAGTGGCCACTCAGAG 180

QY 1213 GCCAGCCTGCAGCGCAACAATGCACACCTCCCAAGACTCCCTTTGTGAGCCCTTG 1272
 DB 181 GCCAGCCTGCAGCGCAACAATGCAGACCTCCCAAGACTCCCTTTGTGAGCCCTTG 240

QY 1273 CTTGCTCCCAAGCCTGTCCATTCGGCAACCAAGTAGGGTCCCAAGATCAGGCCGCTTT 1332
 DB 241 CTTGCTCCCAAGCCTGTCCATTCGGCAACCAAGTAGGGTCCCAAGATCAGGCCGCTTT 300

QY 1333 TACGGGCTGGATTGTACGGTGGCTCCACATGGACTTCTGGTGTCCCGGCTTGCACG 1392
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QY 1393 AAAGGCTGTGAAGATGTCGAGTCTCTGGTGGCTCCAGACTGAGTTCCTTAGCTTCCAG 1452
 DB 361 AAAGGCTGTGAAGATGTCGAGTCTCTGGTGGCTCCAGACTGAGTTCCTTAGCTTCCAG 420

QY 1453 GATGGGGATTTCCCTACCAAGATTTGTGACAGACTATATCCAGTACCAAACTACTGT 1512
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 QY 1813 AACAGTCCAGAGAGGGCCACGGTGGAGCTGGCCCTCCTTAAAA 1858
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 Job time : 7505 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1888.8	99.7	1899	9	BC033010
3	1886	98.0	1886	9	AB051833
4	1856.4	98.0	1889	6	BD192303
5	1811.2	95.6	1892	6	BD136402
6	1258	66.4	1813	4	PIGACRSN
7	1128.2	59.5	1841	4	MUSSP32A
8	1125.4	59.4	1880	10	GPIACRSN
9	937.6	49.5	964	6	BD139445
10	768.4	40.5	2289	6	CQ722423
11	612.2	32.3	1253	10	MUSSP32B
12	610.6	32.2	1524	10	BC011079
13	604.2	31.9	1284	10	BC079212
14	471.8	24.9	56520	9	AC135892
15	471.8	24.9	245880	2	AC079387
16	339	17.9	516	9	HUMYRPA2A04
17	337.2	17.8	522	6	BD179034
18	329.8	17.4	507	6	BD179252
19	282.4	14.9	308	6	BD060281

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23	269.6	14.2	658	10	BC061122	BC061122 Mus muscu
24	258.8	13.7	316	6	AR415759	AR415759 Sequence
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27	124.4	6.6	128	6	AX968632	AX968632 Sequence
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29	106.8	5.6	67573	2	AC122760	AC122760 Mus muscu
30	87.4	4.6	168365	10	AC131653	AC131653 Mus muscu
31	87.4	4.6	179737	2	AC121552	AC121552 Mus muscu
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33	87.4	4.6	251756	10	AC119801	AC119801 Mus muscu
34	86	4.5	199946	10	AC105071	AC105071 Mus muscu
35	85.2	4.5	145678	10	AC131771	AC131771 Mus muscu
36	84.8	4.5	185694	2	AC145610	AC145610 Mus muscu
37	84.8	4.5	236468	2	AC121887	AC121887 Mus muscu
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39	84.2	4.4	203115	2	AC102574	AC102574 Mus muscu
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41	83.2	4.4	157152	10	AC114679	AC114679 Mus muscu
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ALIGNMENTS

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ACCESSION	BD268022				
VERSION	BD268022.1	GI:33077790			
KEYWORDS	JP 2002522081-A/10.				
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ORGANISM	Homo sapiens				
REFERENCE	Bandman,O., Hillman,J.L., Baughn,M.R., Azimzai,Y., Guegler,K.J.,				
AUTHORS	1 (bases 1 to 1912)				
Shih,L.L. and Lu,D.A.M.					
PROTEASES AND ASSOCIATED PROTEINS					
TITLE	Patent: JP 2002522081-A 10 23-JUL-2002;				
JOURNAL	INCYTE PHARMACEUTICALS INC				
COMMENT	OS Homo sapiens (human)				
PN	JP 2002522081-A/10				
PD	23-JUL-2002				
PR	06-AUG-1999 JP 2000565144				
OLGA BANDMAN, JENNIFER L. HILLMAN, MARIH R. BAUGHN, YALDA AZIMZAI, PI					
KARL J. GUEGLER, NELL C. CORLEY, HENRY YUE, TOM Y. TANG, ROOFA REDDY, PI					
CHANDRA PATTERSON, JANICE AU YOUNG, LEO L. SHIH, DYUNG AINA M LU PC					
C12N15/09, A61K38/00, A61K45/00, A61P37/00, A61P43/00, C07K16/40, PC					
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PC A61K37/02					
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FT	/organism='Homo sapiens (human)'				

FEATURES

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ORIGIN

Query Match 99.7%; Score 1890.2; DB 6; Length 1912;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1892; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTAGAGCGGCTTTGTGTCCAGCGGAGCGCGGCGGATCTTCTCCGGCCATGAGGAAGCA 60
 Db 17 GTTAGAGCGGCTTTGTGTCCAGCGGAGCGCGGCGGATCTTCTCCGGCCATGAGGAAGCA 76
 QY 61 GCGGCTGGCTTCTCTCCCTCACTCCGAAAGGCTCTCTGCTCTGCACTGCGCA 120
 Db 77 GCGGCTGGCTTCTCTCCCTCACTCCGAAAGGCTCTCTGCTCTGCACTGCGCA 136
 QY 121 GCCCAGATTTGATCAAGGCCCCCACTCCAGGAGGCGCTCTCTCTCAACGGAATAGAA 180
 Db 137 GCCCAGATTTGATCAAGGCGCTCCACTCCAGGAGGCGCTCTCTCTCAACGGAATAGAA 196
 QY 181 CGCTTCTTGCACTGCTGATCCAACTTGGAAAGGCAAGACTCTGCGCTCTGCGCA 240
 Db 197 CGCTTCTTGCACTGCTGATCCAACTTGGAAAGGCAAGACTCTGCGCTCTGCGCA 256
 QY 241 ACCCAGGCTGCGGAAATCCCACTGCTCAGCTGACCAATATGAAACAGGCTTA 300
 Db 257 ACCCAGGCTGCGGAAATCCCACTGCTCAGCTGACCAATATGAAACAGGCTTA 316
 QY 301 GTGCCGATGATGCTGTCTGCTCCAACTCCCTTAATGCTCTGCTTGAATCTTTCTGC 360
 Db 317 GTGCCGATGATGCTGTCTGCTCCAACTCCCTTAATGCTCTGCTTGAATCTTTCTGC 376
 QY 361 CAGTTCACTCACTACGTTGCTCCAAACGCTCTACTATGCAAGAGAGCTGTGTTC 420
 Db 377 CAGTTCACTCACTACGTTGCTCCAAACGCTCTACTATGCAAGAGAGCTGTGTTC 436
 QY 421 CAGCAGTCTCATTTCTCTCACTCACTCTCAAGAGATGAAAGCTTCACTGAAATC 480
 Db 437 CAGCAGTCTCATTTCTCTCACTCACTCTCAAGAGATGAAAGCTTCACTGAAATC 496
 QY 481 TCACCCACACGATGACTTCCCATCTCACTCCCACTTCAAGTGAAGAGCGCAAGC 540
 Db 497 TCACCCACACGATGACTTCCCATCTCACTCCCACTTCAAGTGAAGAGCGCAAGC 556
 QY 541 TTCAGAGCTTGGGCTGAGAGGCTCAAGCAAGTGAAGAGCTCTTAATCTCTCTTG 600
 Db 557 TTCAGAGCTTGGGCTTGAAGGCTTCAAGCAAGTGAAGAGCTCTTAATCTCTCTTG 616
 QY 601 TCCTTGAAGGCGCAGAGCAAGGCGCAGAGCAAGAGAGAGAGAGAGAGAGAGAG 660
 Db 617 TCCTTGAAGGCGCAGAGCAAGGCGCAGAGCAAGAGAGAGAGAGAGAGAGAGAG 676
 QY 661 CAGGAGCGGCAACAAGAAACAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 Db 677 CAGGAGCGGCAACAAGAAACAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 736
 QY 721 GAAACAG 780
 Db 737 GAAACAG 796
 QY 781 GTGTCTCAGCTGAGCAAGCTCAAGCCCAAGTTTCACTGATCTCTATCTTTCTAC 840
 Db 797 GTGTCTCAGCTGAGCAAGCTCAAGCCCAAGTTTCACTGATCTCTATCTTTCTAC 856
 QY 841 CTTTCTCTTTTCTCTCCCGGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 Db 857 CTTTCTCTTTTCTCTCCCGGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 916
 QY 901 ATCCAGAGCTCATTTGATCAGCCCAAGAAATAGATGAATGAATGAATATATATAGAG 960
 Db 917 ATCCAGAGCTCATTTGATCAGCCCAAGAAATAGATGAATGAATGAATATATATAGAG 976
 QY 961 AACTCTTCTGAGAAACCAAAACCTTGGCAGCTTCTGAGCTGCGCCCAACAGAGGCC 1020
 Db 977 AACTCTTCTGAGAAACCAAAACCTTGGCAGCTTCTGAGCTGCGCCCAACAGAGGCC 1036
 QY 1021 TTGCTGTGTGTGTCTATTCAGATGTGAGAAATCTGCAATCAATACCCCAAGCCAG 1080

Db 1037 TTGCTGTGTGTGTCTATTCAGATGTGAGAAATACCTCAATCAATACCCCAAGCCAG 1096
 QY 1081 GCTTGAAGTCAATGAGAGAGAGATCCCTTGTGAGGAAAGTGTGTGTGACAGCTTT 1140
 Db 1097 GCTTGAAGTCAATGAGAGAGAGATCCCTTGTGAGGAAAGTGTGTGTGACAGCTTT 1156
 QY 1141 GGGCGGCGACACATATCTTACCTGTGCTCTGTGATCTTCTGCTCTTGAAGCTGAGAG 1200
 Db 1157 GGGCGGCGACACATATCTTACCTGTGCTCTGTGATCTTCTGCTCTTGAAGCTGAGAG 1216
 QY 1201 TGCACATCAGAGCGCAGCTGCAAGCGGCAACATGCGACACTCCCAAGAGCTCTTT 1260
 Db 1217 TGCACATCAGAGCGCAGCTGCAAGCGGCAACATGCGACACTCCCAAGAGCTCTTT 1276
 QY 1261 GTACAGCCCTTGTGCTTCTTCCAGAGCTGTGCATGCGCAACAGTAGGAGTCCAGAA 1320
 Db 1277 GTACAGCCCTTGTGCTTCTTCCAGAGCTGTGCATGCGCAACAGTAGGAGTCCAGAA 1336
 QY 1321 TCAGGCGCTTTTACGAGCTGATTTGTAAGTGGGCTCCACATGACCTTCTGTGTGCC 1380
 Db 1337 TCAGGCGCTTTTACGAGCTGATTTGTAAGTGGGCTCCACATGACCTTCTGTGTGCC 1396
 QY 1381 CGGCTTGGCAAGAAAGCTGTGAAGATGTCAGATCTTGGGTGGCTCCAGACTGAGTTTC 1440
 Db 1397 CGGCTTGGCAAGAAAGCTGTGAAGATGTCAGATCTTGGGTGGCTCCAGACTGAGTTTC 1456
 QY 1441 CTAGACTTCCAGATGAGGAGATTTCCCTACCAATTTTGGACACAGATATATCCAGTAC 1500
 Db 1457 CTAGACTTCCAGATGAGGAGATTTCCCTACCAATTTTGGACACAGATATATCCAGTAC 1516
 QY 1501 CCAATCACTGTTCTCTTCAAAAGCCAGAGTGTCTGATGAGAAACCGCAATGGAAGGTG 1560
 Db 1517 CCAATCACTGTTCTCTTCAAAAGCCAGAGTGTCTGATGAGAAACCGCAATGGAAGGTG 1576
 QY 1561 TCCGCAATGATGATGCTGTGCAATGAGACTTCAAGTGTGAGGCTGAGCCCTTGAAGAG 1620
 Db 1577 TCCGCAATGATGATGCTGTGCAATGAGACTTCAAGTGTGAGGCTGAGCCCTTGAAGAG 1636
 QY 1621 GAGGTGTGCTTGTGAGAGAGCCAGAGATTCAGACCTTGAAGTGTGAGGCTGAGTGA 1680
 Db 1637 GAGGTGTGCTTGTGAGAGAGCCAGAGATTCAGACCTTGAAGTGTGAGGCTGAGTGA 1696
 QY 1681 GCTGAGCTGATTCGTCGCCACACCCAGGCCAAGCTGCTTATTTGTTTGAAG 1740
 Db 1697 GCTGAGCTGATTCGTCGCCACACCCAGGCCAAGCTGCTTATTTGTTTGAAG 1756
 QY 1741 ACCCCATTGCTTTCAGAGCTGCTCTTGTGGTCTGTACTCGGCCCTTACATTTCC 1800
 Db 1757 ACCCCATTGCTTTCAGAGCTGCTCTTGTGGTCTGTACTCGGCCCTTACATTTCC 1816
 QY 1801 TTGGGTGAGCAACAGTCCCAAGAGAGGCGACAGTGAAGTGTGCTCTTTAAAGA 1860
 Db 1817 TTGGGTGAGCAACAGTCCCAAGAGAGGCGACAGTGAAGTGTGCTCTTTAAAGA 1876
 QY 1861 TGACTTTACATTAATATGTTGATCTTCAAAAAA 1895
 Db 1877 TGACTTTACATTAATATGTTGATCTTCAAAAAA 1911

RESULT 2
 BC03010 1899 bp mRNA linear PRI 30-JUN-2004
 LOCUS DEINITION
 Homo sapiens acrosin binding protein, mRNA (cdna clone MGC:26629
 IMAGE:482765), complete cds.
 ACCESSION BC03010
 VERSION BC03010.2 GI:34783873
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 1899)

QY	904	CAGGAGCTCAATCGATGAGCCACAGAAATAGATGAAATATATGATGAGAAC	963
Db	901	CAGGAGCTCAATCGATGAGCCACAGAAATAGATGAAATATATGATGAGAAC	960
QY	964	TCCACTGAGAAACCAAAACCCCTGGCAGCTTCCTGCACTGCCCCACACAGAGCCCTTG	1020
Db	961	TCCACTGAGAAACCAAAACCCCTGGCAGCTTCCTGCACTGCCCCACACAGAGCCCTTG	102
QY	1024	CTGTCGTCTGCTAATTCGATTCGTGAGAAATACCTGCATCATATACCCCAAGCCCAAGCC	108
Db	1021	CTGTCGTCTGCTAATTCGATTCGTGAGAAATACCTGCATCATATACCCCAAGCCCAAGCC	108
QY	1084	TGGAAGTACATGAGAGAGAGATCCCTTGTTCCGGAAGTCGATCTGTGACAGCCTTGAG	114
Db	1081	TGGAAGTACATGAGAGAGAGATCCCTTGTTCCGGAAGTCGATCTGTGACAGCCTTGAG	114
QY	1144	CGGCGCACATGTCTAACCCTGTCCTGTGATCTTCCTGCTTCCTGGAAGCTGAGCAGTGC	120
Db	1141	CGGCGCACATGTCTAACCCTGTCCTGTGATCTTCCTGCTTCCTGGAAGCTGAGCAGTGC	120
QY	1204	CACAGAGAGCCAGGCTGACGGGCAACAATGCGACACTCCCAACAAGCTCCCTTGTGC	126
Db	1201	CACAGAGAGCCAGGCTGACGGGCAACAATGCGACACTCCCAACAAGCTCCCTTGTGC	126
QY	1264	AGCCCTTGCTGCTCCACAGCCTGTCATCGGCAACAGGTAGGGTCCCAAGATCA	1323
Db	1261	AGCCCTTGCTGCTCCACAGCCTGTCATCGGCAACAGGTAGGGTCCCAAGATCA	1320
QY	1334	GACCGCTTTACGGGCTGGAATTTGTAACGTGGGCTCAATGACCTTCGTGTGTCGCGG	1383
Db	1331	GACCGCTTTACGGGCTGGAATTTGTAACGTGGGCTCAATGACCTTCGTGTGTCGCGG	1380
QY	1384	CTTGCCACGAAAGCTGTGGAAGTGTCCGAGTCTCGGGTGGCTCAACTGATGATTCCTT	1443
Db	1381	CTTGCCACGAAAGCTGTGGAAGTGTCCGAGTCTCGGGTGGCTCAACTGATGATTCCTT	1440
QY	1444	AGCTTCAGAGATGGGGATTTCCCTACCAAGATTTGTGACACAGATATATCAATACCA	1503
Db	1441	AGCTTCAGAGATGGGGATTTCCCTACCAAGATTTGTGACACAGATATATCAATACCA	1500
QY	1504	AACATCTGTTCTTTCAAAAGCCAGCAGTGTGATGAGAAACCGCAATCGGAAGTGTCC	1563
Db	1501	AACATCTGTTCTTTCAAAAGCCAGCAGTGTGATGAGAAACCGCAATCGGAAGTGTCC	1560
QY	1564	CGCATGAGATGTCTGAGAAATGAGACTTACAGTGGCTGAGCCCTGCAAAATGAGAGAC	1623
Db	1561	CGCATGAGATGTCTGAGAAATGAGACTTACAGTGGCTGAGCCCTGCAAAATGAGAGAC	1620
QY	1624	GTTTGCTCTGATGAGACCAAGATTGACACTTGACTGTAAGCCAGATTCCGATGAGCT	1683
Db	1621	GTTTGCTCTGATGAGACCAAGATTGACACTTGACTGTAAGCCAGATTCCGATGAGCT	1680
QY	1684	GSCGCTAATTCGAGCCACACCCAGCCCAACTGSCCAAGTTCTAATGTTTGAAGCC	1743
Db	1681	GSCGCTAATTCGAGCCACACCCAGCCCAACTGSCCAAGTTCTAATGTTTGAAGCC	1740
QY	1744	CGATTGCTTTAGGGCTGCCCTTCTGAGTCTGTTTACCTGGSCCCCTACATCTTCCTTG	1803
Db	1741	CGATTGCTTTAGGGCTGCCCTTCTGAGTCTGTTTACCTGGSCCCCTACATCTTCCTTG	1800
QY	1804	GGTTGAGCAACAGTCCCAAGAGGGCCACAGTGGAGCTGAGCCCTCTTAAAGATGA	1863
Db	1801	GGTTGAGCAACAGTCCCAAGAGGGCCACAGTGGAGCTGAGCCCTCTTAAAGATGA	1860
QY	1864	CTTTACATAAATGTGATCTTCAAAAAAAA	1895
Db	1861	CTTTACATAAATGTGATCTTCAAAAAAAA	1892

RESULT 3	AB051833	LOCUS	AB051833	1886 bp	mRNA	linear	PR1_15-MAR-2001

DEFINITION	Homo sapiens mRNA for proacrosin binding protein sp32 precursor, complete cds.
ACCESSION	AB051833
VERSION	AB051833.1
KEYWORDS	GI:13366085
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Ukai-Yotsi; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (sites)
AUTHORS	Ono,T., Kuwahigie,T., Harada,N., Noguchi,Y., Saika,T., Nikiyama,N. Aoe,M., Nakamura,S., Higashi,T., Hiraki,A., Wada,H., Kumon,H., Old,J.U. and Nakayama,E.
TITLE	Identification of proacrosin binding protein sp32 precursor as a human cancer/testis antigen
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3282-3287 (2001)
MEDLINE	21145836
PUBMED	11248070
REFERENCE	2 (bases 1 to 1866)
AUTHORS	Ono,T. and Nakayama,E.
TITLE	Direct Submission
JOURNAL	Submitted (27-NOV-2000) Toshio Ono, Okayama University Medical School, Department of Immunology; 2-5-1 Shikata-cho, Okayama, Okayama 700-8558, Japan (E-mail:ono@med.okayama-u.ac.jp, Tel:81-86-235-7192, Fax:81-86-235-7293)
FEATURES	1. location/Qualifiers
source	

ORIGIN

Query Match	99.5%;	Score 1886;	DB 9;	Length 1886
Best Local Similarity	100.0%;	Pred No 0.		

[illegible]

ORIGIN

Query Match 98.0%; Score 1856.4; DB 6; Length 1899;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1879; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

QY 7 GGGCGCTTTGTCACGAGGACGCGGCGAGATCTTCCGGGCGCATAGAGAGCCAGCGCT 66
 Db 1 GGGCGCTTTGTCACGAGGACGCGGCGAGATCTTCCGGGCGCATAGAGAGCCAGCGCT 60
 QY 67 GGGCTTCCTTCCCTCAGCTCCGGAAGGTCGTCCTGCTTGGGACCTGGCGAGCCAG 126
 Db 61 GGGCTTCCTTCCCTCAGCTCCGGAAGGTCGTCCTGCTTGGGACCTGGCGAGCCAG 120
 QY 127 GATTGACATGAGGCGCCCACTCCAGGAGCCCTCTCTCTCTTACCGAATACGAGCTTC 186
 Db 121 GATTGACATGAGGCGCCCACTCCAGGAGCCCTCTCTCTCTTACCGAATACGAGCTTC 180
 QY 187 TTGCGACTGCTGACCTGCAACCTGGAGAGGAGAGACTCTGCGGTCCTGGGACCGAC 246
 Db 181 TTGCGACTGCTGACCTGCAACCTGGAGAGGAGAGACTCTGCGGTCCTGGGACCGAC 240
 QY 247 GGGTCCCGGAAATCCCACTGTCAGCTGGACCAATATGAAACCAAGGCTTTAGTCCC 306
 Db 241 GGGTCCCGGAAATCCCACTGTCAGCTGGACCAATATGAAACCAAGGCTTTAGTCCC 300
 QY 307 GATGGTGTGTCTGCTCCAACTCCCTTATGCTCTGCTTGGTGAATCTTTCTGGCAGTTC 366
 Db 301 GATGGTGTGTCTGCTCCAACTCCCTTATGCTCTGCTTGGTGAATCTTTCTGGCAGTTC 360
 QY 367 ACTGACTACCGTGTCTCCAACTGCTTATGCTTATGCAAGAGAGTCTGTGTTCCAGTCA 426
 Db 361 ACTGACTACCGTGTCTCCAACTGCTTATGCTTATGCAAGAGAGTCTGTGTTCCAGTCA 420
 QY 427 GTCTTATTTCTCACTTACCTCAAGAGAGTGAAGTCTGAGTGAATCTCAACC 486
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 QY 607 GGAGGCGAGGAGAGGCTCAGCAACAGTGAAGAGGCTCTTCACTTCTTGTCTCTG 666
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 QY 787 CAGCTGAG 846
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 QY 967 TACTGAG 1026
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QY 1027 GTGTGTGCTATTTGATCGTGGAGAAATCTGATCATTAACCCCAAGCCAGGCTTGG 1086
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 Db 1081 AAGTATCATGAGAGAGAGATCTTGTGTTTGGAGATCGGTCTGAGACAGCTTGGGCG 1140
 QY 1147 CGACATGTCATCTATGTCCTGTCGATCTTCTGCTTGAAGCTGAGACAGTGGCAC 1206
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 QY 1267 CCTTTCCTTCCCTCCAGAGGCTGTCCATGCGCAACAGTGAAGGTCCTCCAGATCAGC 1326
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 Db 1441 TTCAGAGATGGAGATTTTCCCTTCCAGATTTGTGACACAGACTATTCAGATCCAAAC 1500
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 Db 1561 ATGAGATGTCGAGATGAGATTAAGTGTGCTGAGGCTTGGCAAAAGTGAAGAGCTT 1619
 QY 1627 GTGC-TTGGATGGAGCAGAGATTCAGACCTTGAAGCTTGAAGCCAGTTCGATAGCTG 1685
 Db 1620 GTGC-TTGGATGGAGCAGAGATTCAGACCTTGAAGCTTGAAGCCAGTTCGATAGCTG 1679
 QY 1686 CGTCTATTCGCGCCACACCCCAAGCCCAAGCTTGTCTATTTGTTGAGACCC 1745
 Db 1680 CGTCTATTCGCGCCACACCCCAAGCCCAAGCTTGTCTATTTGTTGAGACCC 1739
 QY 1746 ATTTGCTTTCAGGCTGCCCTTCTGGGCTGTGTTACTGGGCCCTTACTACATTTCTTGG 1805
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 QY 1866 TTACATTAATGTTGATCTTCAAAAAAAA 1895
 Db 1860 TTACATTAATGTTGATCTTCAAAAAAAA 1889

RESULT 5
 BD136402
 LOCUS BD136402
 DEFINITION 95 human secretory proteins.
 ACCESSION BD136402.1 GI:23231347
 VERSION J0200250627-A/89.
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1892)
 AUTHORS Ruben,S.M., Ni,J., Rosen,C.A., Yu,G.L., Young,P.E., Fen,P.,
 Soppet,D.R., Wei,Y.F., Endress,G.A., Duan,R.D., Kyaw,H., Ebner,R.,
 Lafleur,D.W., Olsen,H.S., Shi,Y. and Moore,P.A.
 TITLE 95 human secretory proteins
 JOURNAL Patent: JP 2002506627-A 89 05-MAR-2002;
 HUMAN GENOME SCIENCES INC
 COMMENT OS Homo sapiens (human)
 PN JP 2002506627-A/89
 PD 05-MAR-2002
 PR 18-MAR-1998 JP 2000536733
 PR 19-MAR-1998 US 60/078566,19-MAR-1998 US 60/078576 PR
 19-MAR-1998 US 60/078573,19-MAR-1998 US 60/078574 PR
 19-MAR-1998 US 60/078579,19-MAR-1998 US 60/078578 PR
 19-MAR-1998 US 60/078581,19-MAR-1998 US 60/078577 PR
 19-MAR-1998 US 60/078563,01-APR-1998 US 60/080314 PR
 01-APR-1998 US 60/080312,01-APR-1998 US 60/080313 PI
 M RUBEN, JIAN NI, CRAIG A ROSEN, GUO
 LIANG YU, PAUL E YOUNG,
 PI PING FENG,
 PI DANIEL R SOPPET, YING FEI WEI, GREGORY A ENDRESS, ROXANNE D DUAN,
 PI HLA KYAW,
 PI REINHARD EBNER, DAVID W LAFLEUR, HENRIK S OLSEN, YANGSU SHI, PAUL
 PI A MOORE
 PC C12N15/09,A61K38/00,A61K48/00,A61P43/00,C07K14/47,C07K16/18,
 PC C12N1/15,
 PC C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/53,G01N33/PC
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 PC C12N15/00,A61K37/02,C12N5/00
 CC 95 human secretory proteins
 FH Key Location/Qualifiers
 FT source 1..1892
 FT Location/Qualifiers
 FT /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 95.6%; Score 1811.2; DB 6; Length 1892;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1860; Conservative 0; Mismatches 8; Indels 4; Gaps 4;

QY 24 GGACGGGGGGGATCTTCTCCGCGCATGAGAGCCGCGCTGCTTCCCTACT 83
 DB 13 GGAGCGGAGGATCTTCTCCGCGCATGAGAGCCGCGCTGCTTCCCTACT 72
 QY 84 CCTGAAGTGTCTCTCTGCTCTGCGACTGCGCGAGCCAGGATTGACTAGGCCCC 143
 DB 73 CCGAAGGTGTCTCTCTGCTCTGCGACTGCGCGAGCCAGGATTGACTAGGCCCC 132
 QY 144 CACTCCAGGAGCCCTCTCTCTCTAACAAGTAAAGAAAGCTTCTGCACTGCTGCTCC 203
 DB 133 CACTCCAGGAGCCCTCTCTCTCTAACAAGTAAAGAAAGCTTCTGCACTGCTGCTCC 192
 QY 204 AACCTGGAAGGAGAGACTACCTGCGCTCTCCGTCGCAACCAAGGCTGCGGAATCCAC 263
 DB 193 AACCTGGAAGGAGAGACTACCTGCGCTCTCCGTCGCAACCAAGGCTGCGGAATCCAC 252
 QY 264 ACTGCTCAAGCTGAGCAATATATGAAAAACAGGCTTATGTCGCGATGCTGCTGCTC 323
 DB 253 ACTGCTCAAGCTGAGCAATATATGAAAAACAGGCTTATGTCGCGATGCTGCTGCTC 312
 QY 324 CAACCTCCCTTATGCTCTGCTGTTTGAAGTCTTTCTGCGCACTTCACTACCTGCTC 383
 DB 313 CAACCTCCCTTATGCTCTGCTGTTTGAAGTCTTTCTGCGCACTTCACTACCTGCTC 372
 QY 384 CAACCAAGTCTATGAGCAAGAGAGCTGCTGCTCCAGCAGCTCTATTCCTCACC 443
 DB 373 CAACCAAGTCTATGAGCAAGAGAGCTGCTGCTCCAGCAGCTCTATTCCTCACC 432

QY 444 TAACTCTCAAGAGATAGAGCTTCAGCTGAAGTCTACCAACCAAGATGACTCC 503
 DB 433 TAACACTCTCAAGAGATAGAGCTTCAGCTGAAGTCTACCAACCAAGATGACTCC 492
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 DB 553 CAGCAACAAGTGAAGAGCTCTCAACATCTCTTGTCCCTGGAGAGCCAGAGCAAGC 612
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 DB 613 GCCAGAGCAACAAGAGAGAGAGTGAAGCAAGGAGAGCCAGCAACAAGCAAA 672
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 DB 1032 CTTGAGAAATCTGCTATCTATTAACCCACAGCCAAAGGCTTGAAGTACATGAGAGGA 1091
 QY 1104 GATCTTGTGTTGGGAAAGTGGCTGTGTAACGCTTGGGCGGACACATGCTAACCTG 1163
 DB 1092 GATCTTGTGTTGGGAAAGTGGCTGTGTAACGCTTGGGCGGACACATGCTAACCTG 1151
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 QY 1284 GAGCTGTCCATGGGAAACCAAGTGAAGTCCCAAGATCAAGGCGCTTTTAAAGGCGTGA 1343
 DB 1271 GAGCTGTCCATGGGAAACCAAGTGAAGTCCCAAGATCAAGGCGCTTTTAAAGGCGTGA 1330
 QY 1344 TTTGTACGAGTGGCTCAACATGAGACTTGTGATGAGGCTTGCACAGAAAGCTGTGA 1403
 DB 1331 TTTGTACGAGTGGCTCAACATGAGACTTGTGATGAGGCTTGCACAGAAAGCTGTGA 1390
 QY 1404 AGATGTCCAGTCTCTGAGTGGCTCAACATGAGACTTGTGATGAGGCTTGCACAGATGGGATTT 1463
 DB 1391 AGATGTCCAGTCTCTGAGTGGCTCAACATGAGACTTGTGATGAGGCTTGCACAGATGGGATTT 1449
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 DB 1450 CCTACCAAGATTGAGACAGAGATATACAGTATCCAGTCCCAATACCTGTTCTTCAAAAG 1509
 QY 1524 CCAAGAGTGTCTGATGAGAAACCGCAATCGGAAGTGTCCCGCATGAGATGTCTGAGAA 1583

Db 1510 CCACAGGTCTGATGAGAAACCGCATCCGAGAGTCTCCCGATGAGATGTCGAGAA 1569
 Qy 1584 TGACACTTACAGTCGCGCTGAGACCTTGGCAAAAGTAGAGAGCTTGTCTTGATGAGCA 1643
 Db 1570 TGAACCTTACAGTCGCGCTGAGACCTTGGCAAAAGTAGAGAGCTTGTCTTGATGAGCA 1629
 Qy 1644 GGAAGTACAGACCTTGAAGTACAGTCCGAGTACAGTACGAGCTGATGATGAGCA 1703
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 Qy 1704 CCAGAGCCACCTGCGCCAGCTTCTATGTTTGAAGCCCAATGCTTTGAGGCTGCC 1763
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 Qy 1764 CTCTGGGCTGTTTACTGCGCCCTTCTACATTTCTGTTGAGAGCAAGTCCAG 1823
 Db 1750 CTCTGGGCTGTTTACTGCGCCCTTCTACATTTCTGTTGAGAGCAAGTCCAG 1809
 Qy 1824 AGAGGCGCAGCTGGAGAGCTGCGCCCTTCTTAAAGATGATCTTAAATGTTGATC 1883
 Db 1810 AGAGGCGCAGCTGGAGAGCTGCGCCCTTCTTAAAGATGATCTTAAATGTTGATC 1868
 Qy 1884 TTCAAAAAA 1895
 Db 1869 TTCAAAAAA 1880

RESULT 6

LOCUS PIGACRSN 1813 bp mRNA linear MAM 11-JAN-2003
 DEFINITION Sus scrofa mRNA for sp32 precursor, partial cds.
 ACCESSION D16200
 VERSION D16200.1 GI:475020
 KEYWORDS acrosin.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE

1 (bases 1 to 1813)
 Takenaka, M., Kohno, N., Gerton, G. L. and Arai, Y.
 An acrosomal protein, sp32, in mammalian sperm is a binding protein
 specific for two proacrosins and an acrosin intermediate
 J. Biol. Chem. 269 (13), 10133-10140 (1994)

TITLE

Baba, T., Nida, Y., Michikawa, Y., Kaishibara, S., Kodaira, K.,
 An acrosomal protein, sp32, in mammalian sperm is a binding protein
 specific for two proacrosins and an acrosin intermediate
 J. Biol. Chem. 269 (13), 10133-10140 (1994)

JOURNAL

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 Db 949 TGAAGCCTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1008
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 Db 1720 TCCCTGT 1775
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 Db 1776 CACCTTAAAGAGT 1813

RESULT 7
 MUSSP32A 1841 bp mRNA linear ROD 04-FEB-2003
 LOCUS MUSSP32A
 DEFINITION Mus musculus sp32 mRNA for Proacrosin-binding protein, complete
 cds.
 ACCESSION D17573

VERSION D17573.1 GI:516783
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1841)
 AUTHORS Baba, T.
 TITLE Rodent-specific alternative splicing of RNA for mammalian sperm proacrosin-binding protein, sp32
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1841)
 AUTHORS Baba, T.
 TITLE Direct Submission
 JOURNAL Submitted (10-SEP-1993) Tadashi Baba, University of Tsukuba, Institute of Applied Biochemistry, 1-1-1 Temohai, Tsukuba, Ibaraki 305, Japan (Tel:81-298-53-6632, Fax:81-298-53-6632)
 FEATURES
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Db	310	ATTCTCCCTTATGCTCTCTGCTGTTTGAATCTTCTTGCCAGATTGCTCAATGTTGCTGCTCCA	365
OY	386	ACCACTCTACTATGTCAGAGAGATCTGTGTTTCCACGCAAGTCTTATTTCTCACTTA	445
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Db	667	TAGAAGAAAGCCACAGAACAGAAAGAGCAAGAAAGAAAGAGAGGAGGAAAGCCAAAGC	726
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Db	727	AGGAAGAGGGGACAGGGGACAGAGGCGGGTCTGAGTGCAGTGTCCAGGCTGCAGTCAACT	786
OY	803	CAGAAGCCAAATTCTACTGATCTCTAATCTTCTTAACCTTCCTCTTTTGTCTCCGGG	862
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OY	863	TAGAGAAGTAGAGTCTACTCTTAATGATATAGTGAAGAAATCCAGAGGCTCATTTGATCAG	922
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RESULT 8
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LOCUS      1880 bp      mRNA      linear      ROD 28-JAN-2003
DEFINITION Cavia porcellus mRNA for spj2, complete cds.
ACCESSION  D16203
VERSION     D16203.1  GI:474969
KEYWORDS
SOURCE
ORGANISM   Cavia porcellus (domestic guinea pig)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
REFERENCE
AUTHORS    Baba,T., Nida,Y., Michikawa,Y., Kashiwabara,S., Kodaira,K.,
            Takenaka,M., Kohno,N., Gerton,G.L. and Arai,Y.
            An acrosomal protein, spj2, in mammalian sperm is a binding protein
            specific for two proacrosins and an acrosin intermediate
            J. Biol. Chem. 269 (13), 10133-10140 (1994)
MEDLINE    94193599
PUBMED     8144514
REFERENCE  2 (bases 1 to 1880)
AUTHORS    Baba,T.
TITLE      Direct Submission
JOURNAL    Submitted (06-MAY-1993) Tadashi Baba, University of Tsukuba,
            Institute of Applied Biochemistry, Temohda 1-1-1, Tsukuba, Science
            City, Ibaraki 305, Japan (Tel:81-298-53-6632, Fax:81-298-53-6632)
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polyA_signal
1662..1867

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Query Match      59.4%; Score 1125.4; DB 10; Length 1880;
Best Local Similarity 80.2%; Pred. No. 1.2e-302;
Matches 1377; Conservative 0; Mismatches 321; Indels 19; Gaps 4;

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DB 81 CACTGCTGAGGGTGTCTCTCTCTCTGAGACTGTCTCTGCGCAGAGACTCTTCCCTCGG 140
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QY 677 AACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 736
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QY 737 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 790

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DB 741 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 800
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DB 801 TGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 860
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DB 861 TCAGTCCCGGATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 920
QY 911 TCATTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 970
DB 921 TCATTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 971
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DB 972 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1031
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DB 1032 TTGCTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1091
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DB 1092 ACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1151
QY 1151 ACATGCTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1210
DB 1152 ACATGCTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1211
QY 1211 AGGCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1270
DB 1212 AGGCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1271
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DB 1272 TGTTCCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1331
QY 1331 TTTTACGGGCTGAGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1390
DB 1332 TTTTACGGGCTGAGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1391
QY 1391 CGAAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1450
DB 1392 CAAAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1451
QY 1451 AGAGTGGGATTTTCCCTACCAAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1510
DB 1452 ATTAAGGAGATTTTCCCTACCAAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1511
QY 1511 GTTCTTCAAAAAGTCAAGAGTGTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1570
DB 1512 GTTCTTCAAAAAGTCAAGAGTGTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1571
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QY 1631 TTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1690
DB 1632 TTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1690
QY 1691 ATTCTGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1727
DB 1691 ATTCTGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1727

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RESULT 9
BD139445 964 bp DNA linear PART 18-SEP-2002
LOCUS DEFINITION
BD139445 Extended cDNA of secretory protein.
ACCESSION
BD139445.1 GI:23234390
VERSION

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REFERENCE
1. Bouguet-Lafont, I., Bouteiller, A., and Edwards, J. B. D. M. Extended CDNA of secretory protein. Patent: JP 2002508182-A 197.19-Mar-2003.

COMMENT

FEATURES	Location/Qualifiers
Source	1. .964

ORIGIN

Query Match	49.5%	Score 937.6;	DB 6;	length 964;
Best Local Similarity	99.3%	Pred. No. 3.1e-250;		
Matches 948; Conservative	3.1e-250;			

QY	30	GGGCGGAGTCTTCTCTCGGACATGAGAAAGCCAGCGCTGACTCTCTCTCTCTCACTCCCTGAA	89
Db	2	GGGCGGAGTCTTCTCTCGGACATGAGAAAGCCAGCGCGCTGGCTTCTCTCTCTCACTCCCTGAA	61
QY	90	GGTGTGCTCTCTGCGCTCTGSCACTGSCGCGACGCCAGATTGCACTCAAGGCCCCCACTCC	149
Db	62	GGTGTGCTCTCTGCGCTCTGSCACTGSCGCGACGCCAGATTGCACTCAAGGCCCTCACTCC	121
QY	150	AGGCGGCGCTCTCTCTCTCTCTTACCGAATGCAAGCGCTTCTTGCACTGTGCACTCCAACTCG	209
Db	122	AGGCGGCGCTCTCTCTCTCTCTTACCGAATGCAAGCGCTTCTTGCACTGTGCACTCCAACTCG	181
QY	210	GAAGGCAAGACTACTGTCGCTCGTCCGTCGCAACCCAGGCGCGGGAATTCACACTGCT	269
Db	182	GAAGGCAAGAACTACTGTCGCTCGTCCGTCGCAACCCAGGCGCGGGAATTCACACTGCT	241
QY	270	CGAGCTGAGCAATATGAAACAAGGGTTGTGTCGCCAGTGTGCTGTGCTCCAACT	329
Db	242	CGAGCTGAGCAATATGAAACAAGGGTTGTGTCGCCAGTGTGCTGTGCTCCAACT	301
QY	330	CCCTTATGCGCTCTGCTGGTTGAGTCTTCTGTGCACTTACTACTACCGTGTGCTCCAACT	389
Db	302	CCCTTATGCGCTCTGCTGGTTGAGTCTTCTGTGCACTTACTACTACCGTGTGCTCCAACT	361
QY	390	CGTCTACTATGCGCAAGAGTCTGTCTCCAGCCAGTCTCAATTCTCACTCAAC	449
Db	362	CGTCTACTATGCGCAAGAGTCTGTCTCCAGCCAGTCTCAATTCTCACTCAAC	421
QY	450	TCTCAAGGAGATGAGAAGTCTAGGTGAAGTCTACCAACAC-GATGACTCTCCCACT	508
Db	422	TCTCAAGGAGATGAGAAGTCTAGGTGAAGTCTACCAACACAGATGACTCTCCCACT	481
QY	508	CACCCCACTTCACTGATCAAGAAAGCCAGACTTCCAGCCCTGAGGCTGAGAGGCTCAGCA	568

Db	482	CACCCCACTTCACAGTGACAGAAAGCCAGCACTTCCAGCCTCGGCGCTTAGAGGCTCAGCA	541
OY	569	ACAAAGTGGAAGAGCTCTTCAATCTCTTGTCCCTGGAGGCCAGGACGACGGCAG	628
Db	542	ACAAAGTGGAAGAGCTCTTCAATCTCTTGTCCCTGGAGGCCAGGACGACGGCAG	601
OY	629	AGCAACAAGCAGAGCAGAGGTGAGCAACAGCCAGACGACGACACACAGAACACAGCAGG	688
Db	602	AGCAACAAGCAGAGCAGAGGTGAGCAACAGCCAGACGACGACGACACACAGAACACAGCAGG	661
OY	689	AAGAGGGGCGAGAAACAGGAGACGACAAAGAGAAACAGAAAGAGAGGAGAAAGCAGAGAG	748
Db	662	AAGAGGGGCGAGAAACAGGAGACGAGAAAGAGAAACAGAAAGAGAGGAGAAAGCAGAGAG	721
OY	749	AAGAGCAGGAGGACTAAGAGGAGCGGAGGCGTGATCTCAAGCTGACAGACAGACTTCAGAC	808
Db	722	AAGAGCAGGAGGACTAAGAGGAGCGGAGGCGTGATCTCAAGCTGACAGACAGACTTCAGAC	781
OY	809	CCAAAGTTTCACTCTGAATCTCTATCTTCTAACCCTTCTCTTTTGCTCCCGGGTAGAG	868
Db	782	CCAAAGTTTCACTCTGAATCTCTATCTTCTAACCCTTCTCTTTTGCTCCCGGGTAGAG	841
OY	869	AAGTGAAGCTTACTCTCTATGTATATGAGAGAACTCAGAGAGCTCATTCAGCCGACG	928
Db	842	AAGTGAAGCTTACTCTCTATGTATATGAGAGAACTCAGAGAGCTCATTCAGCCGACG	901
OY	929	AAATGATGAATGAATGAATATATATATAGAACTCTTACGTGGAGAAACCCAAA	993
Db	902	AAATGATGAATGAATGAATATATATATAGAACTCTTACGTGGAGAAACCCAAA	965

RESULT 1C

SEQUENCE	2299 bp	DNA	linear	PAT 03-FEB-2004
DEFINITION	Sequence	8357 from Patent WO02068579.		
ACCESSION	C0722423			

KEYWORDS
CQ/22423.1 GI:42283280

ORGANISM

REFERENCE

TITLE

JOURNAL
Patent: WO 02068579-A 8357 06-SEP-2002;
PE Corporation (NY) (US)

Source

ORIGIN

Query Match	40.5%	Score 768.4;	DB 6;	Length 2299;
Best Local Similarity	99.9%	Pred. No. 6.5e-203;		
Matches 769; Conservative	0;	Mismatches 1;	Indels 0;	

OY	788	AGTGTGACAGACACTCAGAGCCCAAGTTTCACTGTGAATCTCATCTCTTAACCCCTCT	847
Db	356	AGTGTGACAGACACTCAGAGCCCAAGTTTCACTGTGAATCTCATCTCTTAACCCCTCT	
OY	848	CTTTTGCTCCCGGGTACGAGAAATAGTCTCTCTATGATATGGAACATCCAG	907
Db	416	CTTTTGCTCCCGGGTACGAGAAATAGTCTCTCTATGATATGGAACATCCAG	
OY	908	AGCTATTTCATCAGCCCAAGAAATAGTAATGAATATATATATGATGAACTCT	967
Db	476	AGCTATTTCATCAGCCCAAGAAATAGTAATGAATATATATATGATGAACTCT	
OY	968	ACTGAGAAACCAAAACCTTGCGAGCTTCTGAGCTGCCCAACAGAGGCTTGTCTGG	1027

Db	536	ACTGGAGAAACCAAAACCCCTGGAGCCTCTGCACTGCGCCACACAGAGGCTTGTCTGG	595
Qy	1028	TGCTGTGATATTCCATCGTGGAGAAATACCTGCATATTAACCCCAAGCAAGCTCTGGA	1087
Db	596	TGCTGTGATATTCCATCGTGGAGAAATACCTGCATATTAACCCCAAGCAAGCTCTGGA	655
Qy	1088	AGTACATGAGAGAGAGATCCCTGGTTTCGGGAATCCGTCGTGACAGCCCTGGGCGCG	1147
Db	656	AGTACATGAGAGAGAGATCCCTGGTTTCGGGAATCCGTCGTGACAGCCCTGGGCGCG	715
Qy	1148	GACACATGTCACCTGATCCCTCTGTGACTTCTGTCTCTTGAAGCTGGAGAGTGCACCT	1207
Db	716	GACACATGTCACCTGATCCCTCTGTGACTTCTGTCTCTTGAAGCTGGAGAGTGCACCT	775
Qy	1208	CAGAGGCCAGCCTGACGGCGGCAACATGCGACACCTCCACAGACTCCCTTGTGACGC	1267
Db	776	CAGAGGCCAGCCTGACGGCGGCAACATGCGACACCTCCACAGACTCCCTTGTGACGC	835
Qy	1268	CCTTGTCTGCTCCCTCCAGAGCCTGTTCATTCGGACACACAGATAGGGTCCCAAGATAGGC	1322
Db	836	CCTTGTCTGCTCCCTCCAGAGCCTGTTCATTCGGACACACAGATAGGGTCCCAAGATAGGC	895
Qy	1328	GCTTTTACGGGCTGATTTGTATACGGTGGGGCTCCACATGATGATCTTGATGCGCGGCTTG	1387
Db	896	GCTTTTACGGGCTGATTTGTATACGGTGGGGCTCCACATGATGATCTTGATGCGCGGCTTG	955
Qy	1388	CCAGAAAGGCTGTGAMAGATGCCAGATCTCTGGTGGCTCCAGACTGATTCCTTAAGCT	1447
Db	956	CCAGAAAGGCTGTGAMAGATGCCAGATCTCTGGTGGCTCCAGACTGATTCCTTAAGCT	1015
Qy	1448	TCCAGAGATGGGGATTTCCCTTACCAAAGATTTGTGACACAGACTATATCCAGTACCAACT	1507
Db	1016	TCCAGAGATGGGGATTTCCCTTACCAAAGATTTGTGACACAGACTATATCCAGTACCAACT	1075
Qy	1508	ACTGTCTCTTCAAAGACGAGAGTCTGATGAGAAACCGGAATCGGAG	1557
Db	1076	ACTGTCTCTTCAAAGACGAGAGTCTGATGAGAAACCGGAATCGGAG	1125
RESULT 11			
MUSP32B			
LOCUS		1253 bp	linear
DEFINITION	Mus musculus sp32 mRNA for proactosin-binding protein, complete		ROD 04-FEB-2003
ACCESSION	D17574		
VERSION	D17574.1		
KEYWORDS	GI:498163		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 1253)		
REFERENCE	Baba,T.		
AUTHORS	Rodent-specific alternative splicing of RNA for mammalian sperm		
TITLE	proactosin-binding protein, sp32		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 1253)		
TITLE	Baba,T.		
REFERENCE	Direct Submision		
AUTHORS	Submitted (10-SEP-1993) Tadaishi Baba, University of Tsukuba,		
TITLE	Institute of Applied Biochemistry; 1-1-1 Tennohda, Tsukuba,		
JOURNAL	Ibaraki 305, Japan (Tel:81-298-53-6632, Fax:81-298-53-6632)		
FEATURES	Location/Qualifiers		
SOURCE	1..1253		
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	/tissue type="testis"		
	/note="Clones MN2 and MN4"		

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	/protein_id="BA04499.1"
	/db_xref="GI:498164"
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3'UTR	1039..1253
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	1236..1241
	/gene="sp32"
polyA_signal	
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Best Local Similarity	79.3% Pred. No. 2.5e-159;
Matches 780; Conservative	0; Mismatches 186; Indels 15; Gaps 4
Db	26 ACGCGGGCGGATCTTCTCCGCGCATGAGGAAGCAGCGCTGCGCTTCCCTCCATCC 85
OY	
Db	65 ACGGGGGTGGATCTTCCAGGCGCATGATGATCTAGCTGCTGGCTTCTTGATGCTTC 124
OY	86 TGAAGTGTCTGCTCTGCTCTGTGGACCTGCCGACGCCAGAGATTGCACTAGGCTCCCA 145
Db	125 TGAAGTGTCTGCTCTGCTGCGTGAACACCTCTTCCGCTGAGGAAT---CTCAGGCTTCA 181
OY	146 CTCGAGGAGGCGCTCTCTCTCTCTAACCAGATCGAAAGCTTTCTTGCACTGCTGATCCAA 205
Db	182 CTCGAGGAGGCGCTCTCTCTCTCTGTCACGTGATGAAAGCTTTCTTGCGCTCTGACCCAA 241
OY	206 CCTGGAAGGCGAGAACTACTCTGCGGTCCCGTGAACCCAGGCTGCCGATCCCAAC 265
Db	242 CTTGGAAGGCGAGAACCACTGCGCGCTCGCTGCCACCCAGGCTGCCGAACCCCACTC 301
OY	266 TCGTCCAGCTGGACCAATATGAAAAACAAGGCTTAGTGCCTCCGATGTGTCTGTCTCA 325
Db	302 TCGTTCAGTGGATCAATATATGAAAAACAAGGATGTGTAACAGATGTGTCTGTCTCG 361
OY	326 ACCCTCCCTTATGCTCTCTGTTTGAAGTCTTCTGCACTTCACTCACTACCGTTGCTCCA 385
Db	362 ATCTCCCTTATGCTCTCTGTTTGAAGTCTTCTGCACTTCACTCACTACCGTTGCTCCA 421
OY	386 ACCAAGTCTATTATGCCAAGAGAGTCCGTGTTGCCAGCGAGCTCTTATCTTCTCAACCTA 445
Db	422 ACCAAGTCTATTATGCCAAGAGAGTCCGTGTTGCCAGCGAGCTCTTATCTTCTCAACCTA 481
OY	446 AACTCTCAAGAGATAGAACTTCAAGTGAAGTCTCAACCCACAGATGAAGTCTCCCA 505
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OY	506 TCTCACTCCCACTTCACTGATGACAGAACGCCAGACCTTCAGGCTTGCCTGAGAGGCTCA 565
Db	542 TTGTGTCCCAAGCCACAGCCACAGAACCCAGGCTTCCAGCTTGTGGCTGAGGCGCTCA 601
OY	566 GCAACCAAGTGAAGAGCTCTTAACAATCTCTTGTCTCCGAGAGGCGCAGGAGCAAGCGC 625
Db	602 ACAAACAAGTGAAGAGCTCTGACATCTCTTGTCTCCGAGAGGAGCAAGACCAACGA 661
OY	626 CAGAGCAACAAGCAGAGCAGAGTGAAGCAACGCGCAGAGCAGACCGACACAAGAACCAAGC 685
Db	662 GCACTGCGAGCAAGGCCA---GGAGCAGCAACAAGCAGAACCAATCCAAAGACATAAGC 718
OY	686 AGGAAGAGGCGCAAAACAGGAAGC---AGGAAGGGAACAGGAAGAGGGAAGC 742

D	b		476	CCTGGAAGCAGAGAACAACATCGGCCGTCCGGGCACCACCAACGACTGCCGAACCAACCATTC	535
Oy			266	TGTTTCCAGCTTGAGAACCAATATGAAAAACAACGGCTTAGTGCCGATGTGTCTGTCTCCA	325
D	b		536	TGTTTTAATTGGATTCAAATATATAAAAACAACGTAATGTATCACAGATGTGTCTGTCTCG	595
Oy			326	ACCTTCCCCTTAATGACCTCTGAGTTTGATGTCCTTTCTGTGCACATTCACATACCGTGTCTCA	385
D	b		596	ATCTTCCCTTAATGCTTCTCTGTGTGAGTCTTCTGTGCACATTTGTCTCAAGTATCGTTCTCA	655
Oy			386	ACCAAGTCTACTATATGCAAAGAGAGTCCTGTGTGTTCCAGCCAGTCTCTATTTCTCACTTA	445
D	b		656	ACCAATGCTTACTATAGCCAAAGAGGGTCCGGTGTGTCCAAACCGGTCTCAATTCATCCCCA	715
Oy			446	AACCTCTTCAAGAGATAGAGCTTCAAGTGAAGTCTCAACCCACACAGATGACTTCCCCA	505
D	b		716	ACACTCTTCAAGAGAGTGTAGTCTTCAGAGAAATTCCTCCACATTCATGACCAACCCCCA	775
Oy			506	TCTCAACCCCACTTCAACAGTGAACAAGCCCAAGACCTTCACAGCCCGGCTCAGAGACTCA	565
D	b		776	TTGTGTCCCAATGCACACACCAACAGAACACAGGCCCTTCACAGCTTGTGCTGAGCGGCTCA	835
Oy			566	GCAACAACGTGGAAGAGCTCTCAATCTCTGTTCTCCCTGGAGGGCCAGAGACAAGGC	625
D	b		836	ACAACAACGTGAGAGAGCTGTCTGACATATCTTTCTCCCTGGAGGCAAGAACAACAAGA	895
Oy			626	CAGAGCAACACAGAGAGCAGAGAGTGAAGCAACAGCAGAGACCGACACAAGAACAAGC	685
D	b		896	GCACTCCGAGACCAAGGCCA---GGAGCAGCCCAAGCAGAGAGATTCAGAACAATAGC	952
Oy			686	AGGAAGAGGGGCAACAAAACAGAAAGAC--AAAGAAAGAGAACAGAAAGAGAGGAAGC	742
D	b		953	TAGAAGAGGCCACAGAGAGCAAGAAAGCAGAGAAAGAAAGAGAGAGAGAAAGCAAGC	1012
Oy			743	AGGAAGAAAGACAGAGGACCTAAGAGGAGCGGAGGCTGTGTCTCAGTGCAGACAGACT	802
D	b		1013	AGGAAGAGGGGCAAGGAGCAAGAGCGGAGTCTGAGATCAAGTTCACAGCTTCAGATGACT	1072
Oy			803	CAGAGCCCAAGTTTCACTCTGTAATCTATCTTTTAAACCTTCTCTTTGTGTCCCGGG	862
D	b		1073	CAGAGCCCAAGTTTCAATCCCAAGTCACTGTCTTCCAAACCGTCTTTTCACTCCCGGG	1132
Oy			863	TACGAGAAGTAGATCTCTCTCTATGATTAATGAGAGAACATCCAGAGCTCATTTGATAG	922
D	b		1133	TCCAGAGAGTGAAGTCTGCTCATTTGAATGAAGAAATATCCAGAGAGTCAATTCGGTCTG	1192
Oy			923	CCCAAGAAATAGATGAATAATGAATGAATAATATGATGAACAATCCACTGTGAAGAAACAAA	982
D	b		1193	CCCAAGAAATAGATGAATAATGAATGAATGAATGATGATGA-----CTCTGAGAGAACCAAA	1248
Oy			983	ACCCTGGCAGCTTCTGTGCAGCTG 1005	
D	b		1247	GCACCTGGCAGGTACAGGAAATTG 1269	
RESULT 13					
BC079212 1284 bp mRNA linear ROD 03-AUG-2004					
LOCUS BC079212 Rattus norvegicus cDNA clone MGC:94274 IMAGE:7131828, complete cds.					
ACCESSION BC079212 GI:50925776					
VERSION BC079212.1 MI:50925776					
KEYWORDS MGC.					
SOURCE Rattus norvegicus (Norway rat)					
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;					
Rattus.					
REFERENCE 1 (bases 1 to 1284)					
AUTHORS Strauberg,R.L., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,R.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhut,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Ditchenko,L., Marinina,K., Farmer,A.A., Rubin,G.M., Hong,L.,					

ORIGIN	Query Match	Best Local Similarity	Matches
26	ACCGGGCGGATCTTCCCGGCATAGAGGACGCGCGCTTCCTCCCTACTCC	31.9%; Score 604.2; DB 10; Length 1284;	0; Mismatches 203; Indels 12; Gaps 3;
70	ACCGGGAGGATCTTACCAAGAGTATGAACTAGTGTCTACTCTCTCTGATGCTTC	78.1%; Pred. No. 4,4e-157;	0; Mismatches 203; Indels 12; Gaps 3;


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QY      86  TGAAGTGTGCTCTGCTCTGGAACCTGCGCCGACGCCAGATTGCACTGAGGCCCA 145
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QY      146  CTCCAGGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 205
Db      187  CTCCAGGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 246
QY      206  CCTGGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 265
Db      247  CCTGGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 306
QY      266  TGTGTCAGCTGAGCAATATGAAAACCAAGGCTTAGGCGGAGAGAGAGAGAGAGAG 325
Db      307  TGTGTCAGCTGAGCAATATGAAAACCAAGGCTTAGGCGGAGAGAGAGAGAGAGAG 366
QY      326  ACCCTCCCTTAAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 385
Db      367  ACCCTCCCTTAAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 426
QY      386  ACCAGCTCTACTATGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 445
Db      427  ACCAGCTCTACTATGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 486
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QY      506  TCTCAACCCCACTTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 565
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QY      566  GCAACCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 625
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QY      626  CAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 685
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QY      686  AGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 742
Db      727  TAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 786
QY      743  AGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 802
Db      787  AGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 846
QY      803  CAGAGCCCAAGTTCACTGATCTCTATCTCTTAACCTTCTCTCTCTCTCTCTCTCT 862
Db      847  CAGAGCCCAAGTTCACTGATCTCTATCTCTTAACCTTCTCTCTCTCTCTCTCTCT 906
QY      863  TAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 922
Db      907  TCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 966
QY      923  CCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 982
Db      967  CCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY      983  ACCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1005
Db      1021  GCACTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1043

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RESULT 14
 AC135892/c
 LOCUS
 DEFINITION Homo sapiens 12 BAC RP11-433J6 (Roswell) Park Cancer Institute Human
 AC135892
 AC135892.1 GI:24371346
 VERSION

KEYWORDS

HTG.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 56520)
 Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Isman, F.R., Allen, C.,
 Alebrooks, S.L., Amaral, H.C., Are, J.R., Ayele, M., Banks, T.,
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 Direct Submission
 Unpublished
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 Worley, K.C.
 Direct Submission
 Submitted (25-OCT-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc-help@bcm.tmc.edu

TITLE

JOURNAL
 REFERENCE
 AUTHORS
 JOURNAL

COMMENT

CLONE LENGTH: This sequence does not necessarily represent the
 entire insert of this clone. Overlapping regions of clones are only
 sequenced and submitted once, so the sequence for the remainder of
 the insert may be found in the record for the adjacent clones.
 Overlapping clones are noted at the beginning and end of the
 Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches
 of a local database that includes entries from dbSTS, GDB, and
 local mapping efforts.
 Repeats are identified using RepeatMasker (A. Smit and P. Green,
 unpublished) for Human and Mouse sequences.
 Genes and Region of sequence similarity are identified by BLAST

(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found

at URL:
<http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

FEATURES

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ORGANISM

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TITLE
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TITLE
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COMMENT
Unpublished
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Worley, K.C.
Direct Submission
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of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On or before Sep 1, 2000 this sequence version replaced gi:4589937,
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Genome Center
Center: Baylor College of Medicine
Center code: BCM
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Contact: hgsc-help@bcm.tmc.edu
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Center project name: J-11
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Assembly program: Phrap; version 0.990329

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Estimated insert size: 29807; agarose-ftp estimation
Quality coverage: 0x in Q20 bases; agarose-ftp estimation
NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently
consists of 42 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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9173.800 Million cell updates/sec

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapept 60.0

Searched: 1202784 seqs, 818138359 residues

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Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 71	19	1.0	818128	4 US-09-949-016-14548	Sequence 14548, A
C 72	19	1.0	818128	4 US-09-949-016-14549	Sequence 14549, A
C 73	19	1.0	818128	4 US-09-949-016-14550	Sequence 14550, A
C 74	19	1.0	818128	4 US-09-949-016-14551	Sequence 14551, A
C 75	19	1.0	818128	4 US-09-949-016-14552	Sequence 14552, A
C 76	19	1.0	818128	4 US-09-949-016-14553	Sequence 14553, A
C 77	19	1.0	818128	4 US-09-949-016-14554	Sequence 14554, A
C 78	19	1.0	818128	4 US-09-949-016-14555	Sequence 14555, A
C 79	19	1.0	818128	4 US-09-949-016-14556	Sequence 14556, A
C 80	19	1.0	818128	4 US-09-949-016-14557	Sequence 14557, A
C 81	19	1.0	818128	4 US-09-949-016-14558	Sequence 14558, A
C 82	19	1.0	818128	4 US-09-949-016-14559	Sequence 14559, A
C 83	19	1.0	818128	4 US-09-949-016-14560	Sequence 14560, A
C 84	19	1.0	818128	4 US-09-949-016-14561	Sequence 14561, A
C 85	19	1.0	818128	4 US-09-949-016-14562	Sequence 14562, A
C 86	19	1.0	818128	4 US-09-949-016-14564	Sequence 14564, A
C 87	19	1.0	818128	4 US-09-949-016-14565	Sequence 14565, A
C 88	19	1.0	818128	4 US-09-949-016-14566	Sequence 14566, A
C 89	19	1.0	818128	4 US-09-949-016-14567	Sequence 14567, A
C 90	19	0.9	20	4 US-09-758-881-118	Sequence 118, App
C 91	18	0.9	91	4 US-09-513-999C-17556	Sequence 17556, A
C 92	18	0.9	157	4 US-09-513-999C-17602	Sequence 17602, A
C 93	18	0.9	191	4 US-09-513-999C-20801	Sequence 20801, A
C 94	18	0.9	227	4 US-09-702-705-1624	Sequence 1624, Ap
C 95	18	0.9	227	4 US-09-702-705-1624	Sequence 1624, Ap
C 96	18	0.9	227	4 US-09-736-457-1624	Sequence 1624, Ap
C 97	18	0.9	227	4 US-09-736-457-1624	Sequence 1624, Ap
C 98	18	0.9	227	4 US-09-614-124B-1624	Sequence 1624, Ap
C 99	18	0.9	227	4 US-09-614-124B-1641	Sequence 1641, Ap
C 100	18	0.9	227	4 US-09-671-325-1624	Sequence 1624, Ap

C 101	18	0.9	227	4	US-09-671-325-1641	Sequence 1441, Ap	C 174	18	0.9	64190	4	US-09-949-016-14712	Sequence 14712, A
C 102	18	0.9	227	4	US-09-658-824-1524	Sequence 1624, Ap	C 175	18	0.9	64190	4	US-09-949-016-14713	Sequence 14713, A
C 103	18	0.9	227	4	US-09-658-824-1541	Sequence 1641, Ap	C 176	18	0.9	64190	4	US-09-949-016-15413	Sequence 15413, A
C 104	18	0.9	263	4	US-09-902-540-5928	Sequence 5928, Ap	C 177	18	0.9	64190	4	US-09-949-016-15414	Sequence 15414, A
C 105	18	0.9	329	4	US-09-640-211A-1702	Sequence 1702, Ap	C 178	18	0.9	72843	4	US-09-949-016-12574	Sequence 12574, A
C 106	18	0.9	329	4	US-09-640-211A-1742	Sequence 1742, Ap	C 179	18	0.9	75799	4	US-09-949-016-12575	Sequence 12575, A
C 107	18	0.9	378	4	US-09-513-999C-21407	Sequence 21407, Ap	C 180	18	0.9	79595	4	US-09-949-016-15131	Sequence 15131, A
C 108	18	0.9	415	4	US-09-621-976-1691	Sequence 1691, Ap	C 181	18	0.9	80706	4	US-09-949-016-15132	Sequence 15132, A
C 109	18	0.9	425	4	US-09-621-976-1691	Sequence 1691, Ap	C 182	18	0.9	80706	4	US-09-949-016-15133	Sequence 15133, A
C 110	18	0.9	478	4	US-09-621-976-1691	Sequence 1691, Ap	C 183	18	0.9	80706	4	US-09-949-016-15134	Sequence 15134, A
C 111	18	0.9	509	4	US-09-621-976-1691	Sequence 1691, Ap	C 184	18	0.9	80706	4	US-09-949-016-15135	Sequence 15135, A
C 112	18	0.9	509	4	US-09-621-976-1691	Sequence 1691, Ap	C 185	18	0.9	80706	4	US-09-949-016-15136	Sequence 15136, A
C 113	18	0.9	550	4	US-09-918-686-12	Sequence 12, Appl	C 186	18	0.9	86980	4	US-09-949-016-13518	Sequence 13518, A
C 114	18	0.9	601	4	US-09-949-016-29140	Sequence 29140, A	C 187	18	0.9	86980	4	US-09-949-016-13519	Sequence 13519, A
C 115	18	0.9	601	4	US-09-949-016-41095	Sequence 41095, A	C 188	18	0.9	87039	4	US-09-949-016-15344	Sequence 15344, A
C 116	18	0.9	601	4	US-09-949-016-82981	Sequence 82981, A	C 189	18	0.9	87352	4	US-09-949-016-12053	Sequence 12053, A
C 117	18	0.9	601	4	US-09-949-016-168265	Sequence 168265, A	C 190	18	0.9	87352	4	US-09-949-016-12721	Sequence 12721, A
C 118	18	0.9	601	4	US-09-949-016-168266	Sequence 168266, A	C 191	18	0.9	87352	4	US-09-949-016-15692	Sequence 15692, A
C 119	18	0.9	601	4	US-09-949-016-172218	Sequence 172218, A	C 192	18	0.9	87352	4	US-09-949-016-15693	Sequence 15693, A
C 120	18	0.9	611	4	US-09-621-976-1593	Sequence 1593, Ap	C 193	18	0.9	91559	4	US-09-949-016-12581	Sequence 12581, A
C 121	18	0.9	611	4	US-09-621-976-1593	Sequence 1593, Ap	C 194	18	0.9	91559	4	US-09-949-016-13701	Sequence 13701, A
C 122	18	0.9	951	4	US-09-556-419-111	Sequence 111, Ap	C 195	18	0.9	92139	4	US-09-918-686-1	Sequence 1, Appl
C 123	18	0.9	960	4	US-09-556-419-9	Sequence 9, Appl	C 196	18	0.9	94330	4	US-09-949-016-12414	Sequence 12414, A
C 124	18	0.9	1113	4	US-09-252-991A-4148	Sequence 4148, Ap	C 197	18	0.9	94330	4	US-09-949-016-15336	Sequence 15336, A
C 125	18	0.9	1238	4	US-09-397-787-266	Sequence 266, Ap	C 198	18	0.9	94330	4	US-09-949-016-15337	Sequence 15337, A
C 126	18	0.9	1250	4	US-09-370-767-25511	Sequence 25511, A	C 199	18	0.9	95648	4	US-09-949-016-15139	Sequence 15139, A
C 127	18	0.9	1302	4	US-09-352-991A-4458	Sequence 4458, Ap	C 200	18	0.9	98664	4	US-09-949-016-15403	Sequence 15403, A
C 128	18	0.9	1314	4	US-09-352-991A-4290	Sequence 4290, Ap	C 201	18	0.9	99370	4	US-09-949-016-12816	Sequence 12816, A
C 129	18	0.9	1834	4	US-09-902-540-186	Sequence 186, Ap	C 202	18	0.9	100877	4	US-09-949-016-17550	Sequence 17550, A
C 130	18	0.9	1926	2	US-08-978-182-2	Sequence 2, Appl	C 203	18	0.9	100877	4	US-09-949-016-13276	Sequence 13276, A
C 131	18	0.9	1926	2	US-09-805-681-2	Sequence 2, Appl	C 204	18	0.9	102008	4	US-09-949-016-15861	Sequence 15861, A
C 132	18	0.9	1930	4	US-09-270-716D-10159	Sequence 10159, A	C 205	18	0.9	102008	4	US-09-949-016-16167	Sequence 16167, A
C 133	18	0.9	1947	4	US-09-620-312D-1815	Sequence 381, Ap	C 206	18	0.9	102526	4	US-09-949-016-12448	Sequence 12448, A
C 134	18	0.9	2310	4	US-08-416-581B-2	Sequence 2, Appl	C 207	18	0.9	102526	4	US-09-949-016-15409	Sequence 15409, A
C 135	18	0.9	2344	3	US-09-526-542-1	Sequence 1, Appl	C 208	18	0.9	102730	4	US-09-949-016-15410	Sequence 15410, A
C 136	18	0.9	2344	3	US-10-117-087-1	Sequence 1, Appl	C 209	18	0.9	102730	4	US-09-949-016-15411	Sequence 15411, A
C 137	18	0.9	2787	1	US-08-416-581B-3	Sequence 3, Appl	C 210	18	0.9	102730	4	US-09-949-016-15412	Sequence 15412, A
C 138	18	0.9	2787	1	US-08-416-581B-4	Sequence 4, Appl	C 211	18	0.9	102730	4	US-09-949-016-15413	Sequence 15413, A
C 139	18	0.9	2787	3	US-09-288-461-1	Sequence 1, Appl	C 212	18	0.9	102730	4	US-09-949-016-12663	Sequence 12663, A
C 140	18	0.9	2787	3	US-09-087-465-5	Sequence 5, Appl	C 213	18	0.9	102730	4	US-09-949-016-12664	Sequence 12664, A
C 141	18	0.9	2787	4	US-09-972-800A-5	Sequence 1, Appl	C 214	18	0.9	102730	4	US-09-949-016-15409	Sequence 15409, A
C 142	18	0.9	2787	4	US-09-972-800A-5	Sequence 1, Appl	C 215	18	0.9	102730	4	US-09-949-016-15410	Sequence 15410, A
C 143	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 216	18	0.9	102730	4	US-09-949-016-15411	Sequence 15411, A
C 144	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 217	18	0.9	102730	4	US-09-949-016-15412	Sequence 15412, A
C 145	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 218	18	0.9	102730	4	US-09-949-016-15413	Sequence 15413, A
C 146	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 219	18	0.9	102730	4	US-09-949-016-15414	Sequence 15414, A
C 147	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 220	18	0.9	102730	4	US-09-949-016-15415	Sequence 15415, A
C 148	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 221	18	0.9	102730	4	US-09-949-016-15416	Sequence 15416, A
C 149	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 222	18	0.9	102730	4	US-09-949-016-15417	Sequence 15417, A
C 150	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 223	18	0.9	102730	4	US-09-949-016-15418	Sequence 15418, A
C 151	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 224	18	0.9	102730	4	US-09-949-016-15419	Sequence 15419, A
C 152	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 225	18	0.9	102730	4	US-09-949-016-15420	Sequence 15420, A
C 153	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 226	18	0.9	102730	4	US-09-949-016-15421	Sequence 15421, A
C 154	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 227	18	0.9	102730	4	US-09-949-016-15422	Sequence 15422, A
C 155	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 228	18	0.9	102730	4	US-09-949-016-15423	Sequence 15423, A
C 156	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 229	18	0.9	102730	4	US-09-949-016-15424	Sequence 15424, A
C 157	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 230	18	0.9	102730	4	US-09-949-016-15425	Sequence 15425, A
C 158	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 231	18	0.9	102730	4	US-09-949-016-15426	Sequence 15426, A
C 159	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 232	18	0.9	102730	4	US-09-949-016-15427	Sequence 15427, A
C 160	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 233	18	0.9	102730	4	US-09-949-016-15428	Sequence 15428, A
C 161	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 234	18	0.9	102730	4	US-09-949-016-15429	Sequence 15429, A
C 162	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 235	18	0.9	102730	4	US-09-949-016-15430	Sequence 15430, A
C 163	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 236	18	0.9	102730	4	US-09-949-016-15431	Sequence 15431, A
C 164	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 237	18	0.9	102730	4	US-09-949-016-15432	Sequence 15432, A
C 165	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 238	18	0.9	102730	4	US-09-949-016-15433	Sequence 15433, A
C 166	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 239	18	0.9	102730	4	US-09-949-016-15434	Sequence 15434, A
C 167	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 240	18	0.9	102730	4	US-09-949-016-15435	Sequence 15435, A
C 168	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 241	18	0.9	102730	4	US-09-949-016-15436	Sequence 15436, A
C 169	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 242	18	0.9	102730	4	US-09-949-016-15437	Sequence 15437, A
C 170	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 243	18	0.9	102730	4	US-09-949-016-15438	Sequence 15438, A
C 171	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 244	18	0.9	102730	4	US-09-949-016-15439	Sequence 15439, A
C 172	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 245	18	0.9	102730	4	US-09-949-016-15440	Sequence 15440, A
C 173	18	0.9	4084	4	US-09-949-016-15192	Sequence 15192, A	C 246	18	0.9	102730	4	US-09-949-016-15441	Sequence 15441, A

247	18	0.9	156950	4	US-09-949-016-15946	Sequence 15946, A	C 320	17	0.9	483	4	US-09-902-540-3490	Sequence 3490, Ap
C 248	18	0.9	162841	4	US-09-949-016-13733	Sequence 13733, A	C 321	17	0.9	492	4	US-09-621-976-2589	Sequence 2589, Ap
C 249	18	0.9	168104	4	US-09-949-016-12026	Sequence 12026, A	C 322	17	0.9	531	2	US-08-809-185-1	Sequence 1, Appl1
C 250	18	0.9	168105	4	US-09-949-016-16554	Sequence 16554, A	C 323	17	0.9	534	3	US-09-000-630C-24	Sequence 24, Appl
251	18	0.9	168174	4	US-10-071-411A-63	Sequence 63, Appl	C 324	17	0.9	534	3	US-09-000-630C-26	Sequence 26, Appl
252	18	0.9	168273	4	US-10-071-411A-2	Sequence 2, Appl1	C 325	17	0.9	534	3	US-08-862-730C-24	Sequence 24, Appl
253	18	0.9	168394	4	US-09-949-016-13002	Sequence 13002, A	C 326	17	0.9	534	3	US-08-862-730C-26	Sequence 26, Appl
C 254	18	0.9	168575	3	US-09-426-290-1	Sequence 1, Appl1	C 327	17	0.9	534	3	US-09-016-434-1221	Sequence 1221, Ap
C 255	18	0.9	175236	4	US-09-949-016-14353	Sequence 14353, A	C 328	17	0.9	543	1	US-08-422-655-1	Sequence 1, Appl1
C 256	18	0.9	183770	4	US-09-949-016-15494	Sequence 15494, A	C 329	17	0.9	552	4	US-09-621-976-2814	Sequence 2814, Ap
C 257	18	0.9	193303	4	US-09-497-855A-37	Sequence 37, Appl	C 330	17	0.9	588	4	US-09-902-540-8564	Sequence 8564, Ap
C 258	18	0.9	193303	4	US-09-497-855A-44	Sequence 44, Appl	C 331	17	0.9	601	4	US-09-949-016-19017	Sequence 19017, A
259	18	0.9	199471	4	US-09-949-016-14083	Sequence 14083, A	C 332	17	0.9	601	4	US-09-949-016-19018	Sequence 19018, A
C 260	18	0.9	199471	4	US-09-949-016-14083	Sequence 14083, A	C 333	17	0.9	601	4	US-09-949-016-19019	Sequence 19019, A
C 261	18	0.9	199945	4	US-09-949-016-14083	Sequence 14083, A	C 334	17	0.9	601	4	US-09-949-016-19020	Sequence 19020, A
C 262	18	0.9	202001	4	US-09-949-016-15436	Sequence 15436, A	C 335	17	0.9	601	4	US-09-949-016-19021	Sequence 19021, A
C 263	18	0.9	202001	4	US-09-734-674-3	Sequence 3, Appl1	C 336	17	0.9	601	4	US-09-949-016-20287	Sequence 20287, A
264	18	0.9	212139	4	US-09-949-016-13527	Sequence 13527, A	C 337	17	0.9	601	4	US-09-949-016-20288	Sequence 20288, A
C 265	18	0.9	212139	4	US-09-949-016-16085	Sequence 16085, A	C 338	17	0.9	601	4	US-09-949-016-37001	Sequence 37001, A
C 266	18	0.9	225127	4	US-09-949-016-16085	Sequence 16085, A	C 339	17	0.9	601	4	US-09-949-016-41926	Sequence 41926, A
267	18	0.9	225127	4	US-09-949-016-16480	Sequence 16480, A	C 340	17	0.9	601	4	US-09-949-016-47097	Sequence 47097, A
268	18	0.9	228896	4	US-09-949-016-17127	Sequence 17127, A	C 341	17	0.9	601	4	US-09-949-016-47098	Sequence 47098, A
C 269	18	0.9	232547	4	US-09-949-016-16603	Sequence 16603, A	C 342	17	0.9	601	4	US-09-949-016-47099	Sequence 47099, A
C 270	18	0.9	232547	4	US-09-949-016-16420	Sequence 16420, A	C 343	17	0.9	601	4	US-09-949-016-47100	Sequence 47100, A
C 271	18	0.9	237241	4	US-09-949-016-16101	Sequence 16101, A	C 344	17	0.9	601	4	US-09-949-016-47101	Sequence 47101, A
C 272	18	0.9	237863	4	US-09-949-016-13404	Sequence 13404, A	C 345	17	0.9	601	4	US-09-949-016-49792	Sequence 49792, A
C 273	18	0.9	250715	4	US-09-949-016-13294	Sequence 13294, A	C 346	17	0.9	601	4	US-09-949-016-49793	Sequence 49793, A
274	18	0.9	251769	4	US-09-949-016-13185	Sequence 13185, A	C 347	17	0.9	601	4	US-09-949-016-51297	Sequence 51297, A
C 275	18	0.9	251769	4	US-09-949-016-13185	Sequence 13185, A	C 348	17	0.9	601	4	US-09-949-016-51510	Sequence 51510, A
276	18	0.9	251769	4	US-09-949-016-13186	Sequence 13186, A	C 349	17	0.9	601	4	US-09-949-016-51511	Sequence 51511, A
C 277	18	0.9	251769	4	US-09-949-016-13186	Sequence 13186, A	C 350	17	0.9	601	4	US-09-949-016-55577	Sequence 55577, A
278	18	0.9	254366	4	US-09-822-871-3	Sequence 3, Appl1	C 351	17	0.9	601	4	US-09-949-016-55577	Sequence 55577, A
C 279	18	0.9	254778	4	US-09-949-016-12417	Sequence 12417, A	C 352	17	0.9	601	4	US-09-949-016-55577	Sequence 55577, A
C 280	18	0.9	260286	4	US-09-949-016-17037	Sequence 17037, A	C 353	17	0.9	601	4	US-09-949-016-78026	Sequence 78026, A
C 281	18	0.9	260293	4	US-09-949-016-12106	Sequence 12106, A	C 354	17	0.9	601	4	US-09-949-016-83321	Sequence 83321, A
C 282	18	0.9	266748	4	US-09-949-016-13187	Sequence 13187, A	C 355	17	0.9	601	4	US-09-949-016-83322	Sequence 83322, A
C 283	18	0.9	266748	4	US-09-949-016-13187	Sequence 13187, A	C 356	17	0.9	601	4	US-09-949-016-83326	Sequence 83326, A
284	18	0.9	266748	4	US-09-949-016-13188	Sequence 13188, A	C 357	17	0.9	601	4	US-09-949-016-88218	Sequence 88218, A
C 285	18	0.9	266748	4	US-09-949-016-13188	Sequence 13188, A	C 358	17	0.9	601	4	US-09-949-016-88220	Sequence 88220, A
286	18	0.9	268449	4	US-09-949-016-17244	Sequence 17244, A	C 359	17	0.9	601	4	US-09-949-016-102642	Sequence 102642, A
C 287	18	0.9	294836	4	US-09-949-016-15974	Sequence 15974, A	C 360	17	0.9	601	4	US-09-949-016-102642	Sequence 102642, A
C 288	18	0.9	312470	4	US-09-949-016-14043	Sequence 14043, A	C 361	17	0.9	601	4	US-09-949-016-11074	Sequence 11074, A
289	18	0.9	314798	4	US-09-949-016-13559	Sequence 13559, A	C 362	17	0.9	601	4	US-09-949-016-122238	Sequence 122238, A
290	18	0.9	333820	4	US-09-949-016-14139	Sequence 14139, A	C 363	17	0.9	601	4	US-09-949-016-135078	Sequence 135078, A
291	18	0.9	333820	4	US-09-949-016-14139	Sequence 14139, A	C 364	17	0.9	601	4	US-09-949-016-135078	Sequence 135078, A
292	18	0.9	331814	4	US-09-949-016-12008	Sequence 12008, A	C 365	17	0.9	601	4	US-09-949-016-155193	Sequence 155193, A
C 293	18	0.9	336024	4	US-09-949-016-12373	Sequence 12373, A	C 366	17	0.9	601	4	US-09-949-016-155193	Sequence 155193, A
294	18	0.9	336032	4	US-09-949-016-12415	Sequence 12415, A	C 367	17	0.9	601	4	US-09-949-016-169455	Sequence 169455, A
295	18	0.9	353033	4	US-09-949-016-15754	Sequence 15754, A	C 368	17	0.9	601	4	US-09-949-016-175143	Sequence 175143, A
C 296	18	0.9	385136	4	US-09-949-016-16073	Sequence 16073, A	C 369	17	0.9	601	4	US-09-949-016-175260	Sequence 175260, A
C 297	18	0.9	387902	4	US-09-949-016-14543	Sequence 14543, A	C 370	17	0.9	601	4	US-09-949-016-175262	Sequence 175262, A
C 298	18	0.9	390890	4	US-09-949-016-14720	Sequence 14720, A	C 371	17	0.9	601	4	US-09-949-016-177143	Sequence 177143, A
C 299	18	0.9	421883	4	US-09-949-016-12557	Sequence 12557, A	C 372	17	0.9	601	4	US-09-949-016-181656	Sequence 181656, A
C 300	18	0.9	421883	4	US-09-949-016-15473	Sequence 15473, A	C 373	17	0.9	601	4	US-09-949-016-181656	Sequence 181656, A
C 301	18	0.9	451924	4	US-09-949-016-12896	Sequence 12896, A	C 374	17	0.9	601	4	US-09-949-016-181656	Sequence 181656, A
C 302	18	0.9	451925	4	US-09-949-016-17305	Sequence 17305, A	C 375	17	0.9	601	4	US-09-949-016-181658	Sequence 181658, A
303	18	0.9	462589	4	US-09-949-016-12900	Sequence 12900, A	C 376	17	0.9	601	4	US-09-949-016-189520	Sequence 189520, A
304	18	0.9	462589	4	US-09-949-016-12900	Sequence 12900, A	C 377	17	0.9	601	4	US-09-949-016-189521	Sequence 189521, A
C 305	18	0.9	462589	4	US-09-949-016-12900	Sequence 12900, A	C 378	17	0.9	601	4	US-09-949-016-189542	Sequence 189542, A
C 306	18	0.9	636591	4	US-09-949-016-11808	Sequence 11808, A	C 379	17	0.9	601	4	US-09-949-016-189543	Sequence 189543, A
C 307	18	0.9	636591	4	US-09-949-016-13368	Sequence 13368, A	C 380	17	0.9	601	4	US-09-949-016-189561	Sequence 189561, A
C 308	18	0.9	678533	4	US-09-949-016-14577	Sequence 14577, A	C 381	17	0.9	601	4	US-09-949-016-189562	Sequence 189562, A
C 309	18	0.9	678533	4	US-09-949-016-14578	Sequence 14578, A	C 382	17	0.9	601	4	US-09-949-016-200004	Sequence 200004, A
310	18	0.9	767677	4	US-09-949-016-12147	Sequence 12147, A	C 383	17	0.9	601	4	US-09-949-016-200005	Sequence 200005, A
311	18	0.9	767677	4	US-09-949-016-17361	Sequence 17361, A	C 384	17	0.9	601	4	US-09-949-016-200005	Sequence 200005, A
C 312	17	0.9	786431	4	US-09-751-389-3	Sequence 3, Appl1	C 385	17	0.9	759	4	US-09-620-3120-433	Sequence 433, App
C 313	17	0.9	87	1	US-08-476-860-4	Sequence 4, Appl1	C 386	17	0.9	759	4	US-08-998-416-507	Sequence 507, App
C 314	17	0.9	87	2	US-08-910-733-4	Sequence 4, Appl1	C 387	17	0.9	967	4	US-09-799-451-396	Sequence 396, App
C 315	17	0.9	212	4	US-09-513-999C-24036	Sequence 24036, A	C 388	17	0.9	1020	4	US-09-489-0399-4899	Sequence 4899, App
C 316	17	0.9	234	4	US-09-313-994C-6650	Sequence 6650, Ap	C 389	17	0.9	1074	4	US-09-512-363-5	Sequence 5, Appl1
C 317	17	0.9	324	4	US-09-902-540-2768	Sequence 2768, Ap	C 390	17	0.9	1074	4	US-09-176-200-5	Sequence 5, Appl1
318	17	0.9	353	4	US-09-513-999C-15750	Sequence 15750, A	C 391	17	0.9	1074	4	US-09-915-593-5	Sequence 5, Appl1
319	17	0.9	399	4	US-09-543-681A-1067	Sequence 1067, Ap	C 392	17	0.9	1086	4	US-09-248-796A-6002	Sequence 6002, Ap

C 393	17	0.9	1230	3	US-09-572-191-5	Sequence 5, Appl1	C 466	17	0.9	12565	3	US-09-345-217-3	Sequence 3, Appl1
C 394	17	0.9	1230	3	US-09-723-262-5	Sequence 5, Appl1	C 467	17	0.9	12565	4	US-09-845-129-3	Sequence 3, Appl1
C 395	17	0.9	1230	3	US-09-723-219-5	Sequence 5, Appl1	C 468	17	0.9	12565	4	US-09-578-534-17	Sequence 17, Appl1
C 396	17	0.9	1506	4	US-09-252-991A-811	Sequence 811, App	C 469	17	0.9	12565	4	US-09-632-657-3	Sequence 3, Appl1
C 397	17	0.9	1665	4	US-08-812-008-31	Sequence 23, Appl1	C 470	17	0.9	12565	4	US-09-584-950-3	Sequence 3, Appl1
C 398	17	0.9	1683	4	US-09-866-510-23	Sequence 23, Appl1	C 471	17	0.9	12616	4	US-09-849-016-1361	Sequence 3, Appl1
C 399	17	0.9	1710	4	US-09-248-796A-5020	Sequence 5020, Ap	C 472	17	0.9	14037	4	US-09-949-016-1417	Sequence 14217, A
C 400	17	0.9	1789	4	US-09-673-395A-4	Sequence 4, Appl1	C 473	17	0.9	14364	4	US-09-902-540-1111	Sequence 13661, A
C 401	17	0.9	1839	2	US-08-383-744-1	Sequence 1, Appl1	C 474	17	0.9	14572	4	US-10-067-443-20	Sequence 20, Appl1
C 402	17	0.9	1839	2	US-08-383-744-1	Sequence 1, Appl1	C 475	17	0.9	15572	4	US-09-949-016-15384	Sequence 1131, App
C 403	17	0.9	1890	5	PCT-US96-01427-1	Sequence 19, Appl1	C 476	17	0.9	15652	3	US-09-949-016-15384	Sequence 60, Appl1
C 404	17	0.9	1890	3	US-08-935-855-19	Sequence 19, Appl1	C 477	17	0.9	15849	4	US-09-949-016-15384	Sequence 50, Appl1
C 405	17	0.9	1932	4	US-09-949-016-394	Sequence 1526, App	C 478	17	0.9	16321	4	US-09-949-016-15384	Sequence 12490, A
C 406	17	0.9	1932	4	US-09-949-016-1526	Sequence 1526, App	C 479	17	0.9	16738	4	US-09-949-016-15384	Sequence 12490, A
C 407	17	0.9	1947	4	US-09-902-540-6606	Sequence 6606, App	C 480	17	0.9	16738	4	US-09-949-016-15384	Sequence 12490, A
C 408	17	0.9	1951	4	US-09-902-540-6606	Sequence 501, App	C 481	17	0.9	16802	4	US-09-949-016-15384	Sequence 12490, A
C 409	17	0.9	2007	4	US-09-248-796A-4572	Sequence 4572, Ap	C 482	17	0.9	16871	4	US-09-949-016-15384	Sequence 12490, A
C 410	17	0.9	2097	4	US-09-902-540-4742	Sequence 869, App	C 483	17	0.9	16874	4	US-09-949-016-15384	Sequence 12490, A
C 411	17	0.9	2142	4	US-09-252-991A-869	Sequence 4572, Ap	C 484	17	0.9	17128	4	US-09-949-016-15384	Sequence 12490, A
C 412	17	0.9	2387	4	US-09-614-221A-204	Sequence 204, App	C 485	17	0.9	17288	4	US-09-949-016-15384	Sequence 12490, A
C 413	17	0.9	2409	4	US-09-902-540-459	Sequence 2268, App	C 486	17	0.9	18391	4	US-09-949-016-15384	Sequence 12490, A
C 414	17	0.9	3134	4	US-09-866-510-13	Sequence 439, App	C 487	17	0.9	18798	4	US-09-949-016-15384	Sequence 12490, A
C 415	17	0.9	3321	4	US-09-866-510-15	Sequence 13, Appl1	C 488	17	0.9	19056	3	US-09-272-032-8	Sequence 8, Appl1
C 416	17	0.9	3321	4	US-09-866-510-15	Sequence 13, Appl1	C 489	17	0.9	19056	3	US-09-272-032-8	Sequence 8, Appl1
C 417	17	0.9	3321	4	US-09-866-510-15	Sequence 15, Appl1	C 490	17	0.9	23975	4	US-09-443-218-8	Sequence 8, Appl1
C 418	17	0.9	3321	4	US-09-866-510-15	Sequence 15, Appl1	C 491	17	0.9	25254	4	US-09-949-016-17126	Sequence 8, Appl1
C 419	17	0.9	3321	4	US-09-866-510-15	Sequence 19, Appl1	C 492	17	0.9	25254	4	US-09-949-016-17126	Sequence 17126, A
C 420	17	0.9	3422	4	US-09-949-016-1919	Sequence 1919, Ap	C 493	17	0.9	25882	4	US-09-949-016-14330	Sequence 14339, A
C 421	17	0.9	3490	4	US-09-949-016-1919	Sequence 880, App	C 494	17	0.9	25882	4	US-09-949-016-14330	Sequence 14339, A
C 422	17	0.9	4076	4	US-09-573-080A-632	Sequence 62, Appl1	C 495	17	0.9	26210	4	US-09-949-016-17133	Sequence 14391, A
C 423	17	0.9	4076	4	US-09-573-080A-632	Sequence 839, Ap	C 496	17	0.9	26210	4	US-09-949-016-17133	Sequence 14391, A
C 424	17	0.9	4163	4	US-09-949-016-4839	Sequence 748, App	C 497	17	0.9	28058	4	US-09-949-016-17168	Sequence 17168, A
C 425	17	0.9	4308	4	US-09-949-016-748	Sequence 8, Appl1	C 498	17	0.9	28129	4	US-09-949-016-17168	Sequence 17168, A
C 426	17	0.9	4308	4	US-09-949-016-748	Sequence 8, Appl1	C 499	17	0.9	28933	4	US-09-949-016-17168	Sequence 17168, A
C 427	17	0.9	4308	4	US-09-949-016-748	Sequence 8, Appl1	C 500	17	0.9	29977	4	US-09-949-016-16095	Sequence 16095, A
C 428	17	0.9	4328	1	US-08-322-742-12	Sequence 12, Appl1	C 501	17	0.9	31719	4	US-09-949-016-17452	Sequence 17452, A
C 429	17	0.9	4465	1	US-08-180-195-1	Sequence 1, Appl1	C 502	17	0.9	31719	4	US-09-949-016-17452	Sequence 17452, A
C 430	17	0.9	4465	1	US-08-477-329-1	Sequence 1, Appl1	C 503	17	0.9	32065	4	US-09-949-016-16226	Sequence 16226, A
C 431	17	0.9	4465	2	US-08-477-329-1	Sequence 1, Appl1	C 504	17	0.9	32065	4	US-09-949-016-16226	Sequence 16226, A
C 432	17	0.9	4465	3	US-08-980-400-1	Sequence 1, Appl1	C 505	17	0.9	32066	4	US-09-949-016-16226	Sequence 16226, A
C 433	17	0.9	4465	3	US-08-980-400-1	Sequence 1, Appl1	C 506	17	0.9	32666	4	US-09-949-016-16086	Sequence 16086, A
C 434	17	0.9	4465	3	US-09-583-459A-1	Sequence 1, Appl1	C 507	17	0.9	34408	4	US-09-949-016-16086	Sequence 16086, A
C 435	17	0.9	4465	3	US-09-583-459A-1	Sequence 1, Appl1	C 508	17	0.9	35493	4	US-09-949-016-16086	Sequence 16086, A
C 436	17	0.9	4465	3	US-09-583-459A-1	Sequence 1, Appl1	C 509	17	0.9	36633	4	US-09-949-016-16086	Sequence 16086, A
C 437	17	0.9	4465	3	US-09-583-459A-1	Sequence 15, Appl1	C 510	17	0.9	36821	4	US-09-949-016-16086	Sequence 16086, A
C 438	17	0.9	4757	3	US-08-322-742-15	Sequence 1, Appl1	C 511	17	0.9	37004	4	US-09-949-016-16086	Sequence 16086, A
C 439	17	0.9	4757	3	US-09-723-262-1	Sequence 1, Appl1	C 512	17	0.9	37004	4	US-09-949-016-16086	Sequence 16086, A
C 440	17	0.9	5102	1	US-09-723-219-1	Sequence 1, Appl1	C 513	17	0.9	39299	4	US-09-949-016-16255	Sequence 16255, A
C 441	17	0.9	5102	1	US-08-494-168-1	Sequence 1, Appl1	C 514	17	0.9	43018	4	US-09-949-016-16255	Sequence 16255, A
C 442	17	0.9	5172	4	US-09-949-016-5785	Sequence 5785, Ap	C 515	17	0.9	43018	4	US-09-949-016-16255	Sequence 16255, A
C 443	17	0.9	5427	2	US-08-168-917-1	Sequence 1, Appl1	C 516	17	0.9	47799	4	US-09-949-016-17330	Sequence 17330, A
C 444	17	0.9	5427	2	US-08-460-510-1	Sequence 1, Appl1	C 517	17	0.9	48556	4	US-09-949-016-13363	Sequence 13363, A
C 445	17	0.9	5427	2	US-08-460-490-1	Sequence 1, Appl1	C 518	17	0.9	48556	4	US-09-949-016-13363	Sequence 13363, A
C 446	17	0.9	5427	3	US-08-461-728-3	Sequence 3, Appl1	C 519	17	0.9	49301	4	US-09-949-016-1167	Sequence 1167, A
C 447	17	0.9	5427	3	US-08-461-917-3	Sequence 3, Appl1	C 520	17	0.9	49301	4	US-09-949-016-1167	Sequence 1167, A
C 448	17	0.9	5427	4	US-08-464-436-3	Sequence 3, Appl1	C 521	17	0.9	49829	4	US-09-949-016-12458	Sequence 12458, A
C 449	17	0.9	5427	4	US-08-464-436-3	Sequence 3, Appl1	C 522	17	0.9	50453	4	US-09-949-016-16442	Sequence 16442, A
C 450	17	0.9	5427	5	PCT-US92-00730-1	Sequence 1, Appl1	C 523	17	0.9	51272	4	US-09-949-016-16442	Sequence 16442, A
C 451	17	0.9	5427	5	PCT-US92-00730-1	Sequence 1, Appl1	C 524	17	0.9	51272	4	US-09-949-016-16442	Sequence 16442, A
C 452	17	0.9	5570	4	US-09-023-655-1193	Sequence 1193, Ap	C 525	17	0.9	53769	4	US-09-949-016-16002	Sequence 16002, A
C 453	17	0.9	5727	4	US-09-628-188A-1	Sequence 9, Appl1	C 526	17	0.9	68032	4	US-09-949-016-16803	Sequence 16803, A
C 454	17	0.9	5824	4	US-09-561-818A-1	Sequence 1, Appl1	C 527	17	0.9	71645	4	US-09-949-016-16219	Sequence 16219, A
C 455	17	0.9	6625	4	US-09-949-016-13534	Sequence 13534, A	C 528	17	0.9	71645	4	US-09-949-016-16219	Sequence 16219, A
C 456	17	0.9	6728	4	US-09-949-016-13534	Sequence 13534, A	C 529	17	0.9	76281	4	US-09-949-016-12708	Sequence 12708, A
C 457	17	0.9	7890	4	US-09-949-016-2425	Sequence 2425, Ap	C 530	17	0.9	79756	4	US-09-949-016-17537	Sequence 17537, A
C 458	17	0.9	9044	4	US-09-949-016-14661	Sequence 14661, A	C 531	17	0.9	81433	4	US-09-949-016-17537	Sequence 17537, A
C 459	17	0.9	9127	4	US-09-949-016-13515	Sequence 13515, A	C 532	17	0.9	84227	4	US-09-949-016-17334	Sequence 17334, A
C 460	17	0.9	9508	4	US-09-949-016-13515	Sequence 13515, A	C 533	17	0.9	84227	4	US-09-949-016-17334	Sequence 17334, A
C 461	17	0.9	9508	4	US-09-949-016-13515	Sequence 13515, A	C 534	17	0.9	84227	4	US-09-949-016-17334	Sequence 17334, A
C 462	17	0.9	11382	4	US-09-902-540-904	Sequence 904, App	C 535	17	0.9	85439	4	US-09-949-016-16590	Sequence 16590, A
C 463	17	0.9	11382	4	US-09-949-016-14245	Sequence 14245, A	C 536	17	0.9	92505	4	US-09-949-016-14018	Sequence 14018, A
C 464	17	0.9	12138	4	US-09-949-016-14245	Sequence 14245, A	C 537	17	0.9	93398	4	US-09-949-016-14245	Sequence 14245, A
C 465	17	0.9	12423	4	US-09-949-016-14959	Sequence 14959, A	C 538	17	0.9	95621	4	US-09-949-016-13237	Sequence 13237, A
	17	0.9	12438	4	US-09-949-016-16581	Sequence 16581, A							

539	17	0.9	97221	4	US-09-949-016-12755	Sequence 12755, A	612	16	0.8	95	1	US-08-180-195-17	Sequence 17, Appl
540	17	0.9	103772	4	US-09-949-016-13058	Sequence 13058, A	613	16	0.8	95	1	US-08-477-329-16	Sequence 16, Appl
541	17	0.9	107800	4	US-09-949-016-13118	Sequence 13118, A	614	16	0.8	95	1	US-08-477-329-16	Sequence 16, Appl
542	17	0.9	111677	4	US-09-949-016-16966	Sequence 16966, A	615	16	0.8	95	2	US-08-475-458-16	Sequence 16, Appl
543	17	0.9	116425	4	US-09-949-016-11809	Sequence 11809, A	616	16	0.8	95	2	US-08-475-458-16	Sequence 16, Appl
544	17	0.9	119032	4	US-09-949-016-12160	Sequence 12160, A	617	16	0.8	95	3	US-08-980-400-17	Sequence 17, Appl
545	17	0.9	119032	4	US-09-949-016-17268	Sequence 17268, A	618	16	0.8	95	3	US-08-980-400-17	Sequence 17, Appl
546	17	0.9	121427	4	US-09-949-016-11950	Sequence 11950, A	619	16	0.8	95	3	US-09-583-459A-16	Sequence 16, Appl
547	17	0.9	121433	4	US-09-949-016-13220	Sequence 13220, A	620	16	0.8	95	3	US-09-583-459A-16	Sequence 16, Appl
548	17	0.9	125672	4	US-09-949-016-16966	Sequence 16966, A	621	16	0.8	95	3	US-09-583-459A-16	Sequence 16, Appl
549	17	0.9	128779	4	US-09-487-855A-38	Sequence 38, Appl	622	16	0.8	95	3	US-09-583-459A-16	Sequence 16, Appl
550	17	0.9	130724	4	US-09-949-016-13753	Sequence 13753, A	623	16	0.8	95	3	US-09-583-459A-16	Sequence 16, Appl
551	17	0.9	130971	4	US-09-949-016-14205	Sequence 14205, A	624	16	0.8	95	3	US-09-583-459A-16	Sequence 16, Appl
552	17	0.9	143550	4	US-09-949-016-14113	Sequence 14113, A	625	16	0.8	95	3	US-09-435-059-17	Sequence 17, Appl
553	17	0.9	146307	4	US-09-949-016-14881	Sequence 14881, A	626	16	0.8	95	3	US-09-435-059-17	Sequence 17, Appl
554	17	0.9	146307	4	US-09-949-016-14882	Sequence 14882, A	627	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
555	17	0.9	146307	4	US-09-949-016-14883	Sequence 14883, A	628	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
556	17	0.9	146307	4	US-09-949-016-14884	Sequence 14884, A	629	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
557	17	0.9	146307	4	US-09-949-016-14885	Sequence 14885, A	630	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
558	17	0.9	146307	4	US-09-949-016-14886	Sequence 14886, A	631	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
559	17	0.9	146307	4	US-09-949-016-14887	Sequence 14887, A	632	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
560	17	0.9	146307	4	US-09-949-016-14888	Sequence 14888, A	633	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
561	17	0.9	148405	4	US-09-949-016-11747	Sequence 11747, A	634	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
562	17	0.9	148405	4	US-09-949-016-12835	Sequence 12835, A	635	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
563	17	0.9	148405	4	US-09-949-016-12836	Sequence 12836, A	636	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
564	17	0.9	148405	4	US-09-949-016-12837	Sequence 12837, A	637	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
565	17	0.9	149543	4	US-09-949-016-15947	Sequence 15947, A	638	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
566	17	0.9	150409	4	US-09-949-016-12928	Sequence 12928, A	639	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
567	17	0.9	150409	4	US-09-949-016-12929	Sequence 12929, A	640	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
568	17	0.9	152524	4	US-09-949-016-12663	Sequence 12663, A	641	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
569	17	0.9	152524	4	US-09-949-016-13194	Sequence 13194, A	642	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
570	17	0.9	161124	4	US-09-949-016-11760	Sequence 11760, A	643	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
571	17	0.9	174039	4	US-09-949-016-12610	Sequence 12610, A	644	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
572	17	0.9	174039	4	US-09-949-016-13880	Sequence 13880, A	645	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
573	17	0.9	177293	4	US-09-949-016-16513	Sequence 16513, A	646	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
574	17	0.9	193169	4	US-09-949-016-15091	Sequence 15091, A	647	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
575	17	0.9	194889	4	US-09-949-016-15654	Sequence 15654, A	648	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
576	17	0.9	218940	4	US-09-949-016-17539	Sequence 17539, A	649	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
577	17	0.9	227390	4	US-09-949-016-12201	Sequence 12201, A	650	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
578	17	0.9	227391	4	US-09-949-016-13365	Sequence 13365, A	651	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
579	17	0.9	250352	4	US-09-949-016-14724	Sequence 14724, A	652	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
580	17	0.9	256171	4	US-09-949-016-12822	Sequence 12822, A	653	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
581	17	0.9	256176	4	US-09-949-016-15524	Sequence 15524, A	654	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
582	17	0.9	278866	4	US-09-949-016-13922	Sequence 13922, A	655	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
583	17	0.9	278866	4	US-09-949-016-13923	Sequence 13923, A	656	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
584	17	0.9	278866	4	US-09-949-016-13924	Sequence 13924, A	657	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
585	17	0.9	278866	4	US-09-949-016-13925	Sequence 13925, A	658	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
586	17	0.9	278866	4	US-09-949-016-13926	Sequence 13926, A	659	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
587	17	0.9	278866	4	US-09-949-016-14699	Sequence 14699, A	660	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
588	17	0.9	278866	4	US-09-949-016-14700	Sequence 14700, A	661	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
589	17	0.9	278866	4	US-09-949-016-14701	Sequence 14701, A	662	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
590	17	0.9	278866	4	US-09-949-016-14702	Sequence 14702, A	663	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
591	17	0.9	278866	4	US-09-949-016-14703	Sequence 14703, A	664	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
592	17	0.9	392000	4	US-10-027-983-11	Sequence 11, Appl	665	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
593	17	0.9	392000	4	US-10-027-983-11	Sequence 11, Appl	666	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
594	17	0.9	421118	4	US-09-949-016-16297	Sequence 16297, A	667	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
595	17	0.9	4403765	3	US-09-790-988A-1	Sequence 1, Appl	668	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
596	17	0.9	4403765	3	US-09-103-840A-2	Sequence 2, Appl	669	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
597	17	0.9	4411529	3	US-09-103-840A-1	Sequence 1, Appl	670	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
598	17	0.8	20	1	US-08-480-784-9	Sequence 9, Appl	671	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
599	16	0.8	20	1	US-08-483-553-9	Sequence 9, Appl	672	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
600	16	0.8	20	1	US-08-487-002-9	Sequence 9, Appl	673	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
601	16	0.8	20	1	US-08-483-554B-9	Sequence 9, Appl	674	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
602	16	0.8	20	1	US-08-488-011B-9	Sequence 9, Appl	675	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
603	16	0.8	20	1	US-08-850-727-9	Sequence 9, Appl	676	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
604	16	0.8	20	5	PCT-US95-10202-9	Sequence 9, Appl	677	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
605	16	0.8	20	5	PCT-US95-10202-9	Sequence 9, Appl	678	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
606	16	0.8	20	5	PCT-US95-10202-9	Sequence 9, Appl	679	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
607	16	0.8	25	4	US-09-396-1966C-30034	Sequence 30034, A	680	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
608	16	0.8	28	1	US-08-723-896C-15	Sequence 15, Appl	681	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
609	16	0.8	28	3	US-08-424-797A-15	Sequence 15, Appl	682	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
610	16	0.8	84	1	US-08-246-583-7	Sequence 7, Appl	683	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A
611	16	0.8	95	1	US-08-180-195-16	Sequence 16, Appl	684	16	0.8	95	3	US-09-513-999C-18689	Sequence 18689, A

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C 690	16	0.8	601	4	US-09-949-016-20116	Sequence 20116, A
C 691	16	0.8	601	4	US-09-949-016-20399	Sequence 20399, A
C 692	16	0.8	601	4	US-09-949-016-21548	Sequence 21548, A
C 693	16	0.8	601	4	US-09-949-016-21549	Sequence 21549, A
C 694	16	0.8	601	4	US-09-949-016-26532	Sequence 26532, A
C 695	16	0.8	601	4	US-09-949-016-27931	Sequence 27931, A
C 696	16	0.8	601	4	US-09-949-016-29021	Sequence 29021, A
C 697	16	0.8	601	4	US-09-949-016-29022	Sequence 29022, A
C 698	16	0.8	601	4	US-09-949-016-29023	Sequence 29023, A
C 699	16	0.8	601	4	US-09-949-016-29024	Sequence 29024, A
C 700	16	0.8	601	4	US-09-949-016-29025	Sequence 29025, A
C 701	16	0.8	601	4	US-09-949-016-29026	Sequence 29026, A
C 702	16	0.8	601	4	US-09-949-016-29419	Sequence 29419, A
C 703	16	0.8	601	4	US-09-949-016-31842	Sequence 31842, A
C 704	16	0.8	601	4	US-09-949-016-31843	Sequence 31843, A
C 705	16	0.8	601	4	US-09-949-016-36934	Sequence 36934, A
C 706	16	0.8	601	4	US-09-949-016-37893	Sequence 37893, A
C 707	16	0.8	601	4	US-09-949-016-38379	Sequence 38379, A
C 708	16	0.8	601	4	US-09-949-016-39350	Sequence 39350, A
C 709	16	0.8	601	4	US-09-949-016-39352	Sequence 39352, A
C 710	16	0.8	601	4	US-09-949-016-39414	Sequence 39414, A
C 711	16	0.8	601	4	US-09-949-016-46984	Sequence 46984, A
C 712	16	0.8	601	4	US-09-949-016-47092	Sequence 47092, A
C 713	16	0.8	601	4	US-09-949-016-47540	Sequence 47540, A
C 714	16	0.8	601	4	US-09-949-016-47541	Sequence 47541, A
C 715	16	0.8	601	4	US-09-949-016-48081	Sequence 48081, A
C 716	16	0.8	601	4	US-09-949-016-48476	Sequence 48476, A
C 717	16	0.8	601	4	US-09-949-016-48729	Sequence 48729, A
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C 719	16	0.8	601	4	US-09-949-016-52558	Sequence 52558, A
C 720	16	0.8	601	4	US-09-949-016-53369	Sequence 53369, A
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C 722	16	0.8	601	4	US-09-949-016-53421	Sequence 53421, A
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C 724	16	0.8	601	4	US-09-949-016-55644	Sequence 55644, A
C 725	16	0.8	601	4	US-09-949-016-55845	Sequence 55845, A
C 726	16	0.8	601	4	US-09-949-016-58466	Sequence 58466, A
C 727	16	0.8	601	4	US-09-949-016-60385	Sequence 60385, A
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C 730	16	0.8	601	4	US-09-949-016-60433	Sequence 60433, A
C 731	16	0.8	601	4	US-09-949-016-60848	Sequence 60848, A
C 732	16	0.8	601	4	US-09-949-016-62589	Sequence 62589, A
C 733	16	0.8	601	4	US-09-949-016-62590	Sequence 62590, A
C 734	16	0.8	601	4	US-09-949-016-62780	Sequence 62780, A
C 735	16	0.8	601	4	US-09-949-016-62781	Sequence 62781, A
C 736	16	0.8	601	4	US-09-949-016-62787	Sequence 62

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836	16	0.8	601	4	US-09-949-016-114215	Sequence 114215,	909	16	0.8	601	4	US-09-949-016-172097	Sequence 172097,
837	16	0.8	601	4	US-09-949-016-114383	Sequence 114383,	c 910	16	0.8	601	4	US-09-949-016-172623	Sequence 172623,
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855	16	0.8	601	4	US-09-949-016-123371	Sequence 123371,	c 928	16	0.8	601	4	US-09-949-016-181652	Sequence 181652,
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863	16	0.8	601	4	US-09-949-016-124766	Sequence 124766,	936	16	0.8	601	4	US-09-949-016-184962	Sequence 184962,
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875	16	0.8	601	4	US-09-949-016-138084	Sequence 138084,	948	16	0.8	601	4	US-09-949-016-195473	Sequence 195473,
c 876	16	0.8	601	4	US-09-949-016-138720	Sequence 138720,	c 949	16	0.8	601	4	US-09-949-016-195928	Sequence 195928,
877	16	0.8	601	4	US-09-949-016-138721	Sequence 138721,	950	16	0.8	601	4	US-09-949-016-196812	Sequence 196812,
c 878	16	0.8	601	4	US-09-949-016-138722	Sequence 138722,	951	16	0.8	601	4	US-09-949-016-196840	Sequence 196840,
c 879	16	0.8	601	4	US-09-949-016-139151	Sequence 139151,	952	16	0.8	601	4	US-09-949-016-201232	Sequence 201232,
c 880	16	0.8	601	4	US-09-949-016-139654	Sequence 139654,	953	16	0.8	601	4	US-09-949-016-201865	Sequence 201865,
c 881	16	0.8	601	4	US-09-949-016-141629	Sequence 141629,	c 954	16	0.8	601	4	US-09-949-016-202979	Sequence 202979,
c 882	16	0.8	601	4	US-09-949-016-141629	Sequence 141629,	c 955	16	0.8	601	4	US-09-949-016-204389	Sequence 204389,
c 883	16	0.8	601	4	US-09-949-016-141630	Sequence 141630,	956	16	0.8	601	4	US-09-949-016-204551	Sequence 204551,
c 884	16	0.8	601	4	US-09-949-016-148942	Sequence 148942,	957	16	0.8	601	4	US-09-949-016-205099	Sequence 205099,
c 885	16	0.8	601	4	US-09-949-016-149009	Sequence 149009,	958	16	0.8	601	4	US-09-949-016-205503	Sequence 205503,
c 886	16	0.8	601	4	US-09-949-016-149076	Sequence 149076,	959	16	0.8	601	4	US-09-949-016-205504	Sequence 205504,
c 887	16	0.8	601	4	US-09-949-016-149143	Sequence 149143,	960	16	0.8	601	4	US-09-949-016-205505	Sequence 205505,
c 888	16	0.8	601	4	US-09-949-016-151918	Sequence 151918,	c 961	16	0.8	601	4	US-09-949-016-205545	Sequence 205545,
889	16	0.8	601	4	US-09-949-016-152483	Sequence 152483,	c 962	16	0.8	601	4	US-09-949-016-205546	Sequence 205546,
890	16	0.8	601	4	US-09-949-016-152484	Sequence 152484,	c 963	16	0.8	601	4	US-09-949-016-206011	Sequence 206011,
891	16	0.8	601	4	US-09-949-016-152779	Sequence 152779,	c 964	16	0.8	601	4	US-09-949-016-206016	Sequence 206016,
c 892	16	0.8	601	4	US-09-949-016-156049	Sequence 156049,	c 965	16	0.8	601	4	US-09-949-016-206474	Sequence 206474,
c 893	16	0.8	601	4	US-09-949-016-156050	Sequence 156050,	c 966	16	0.8	601	4	US-09-949-016-206535	Sequence 206535,
c 894	16	0.8	601	4	US-09-949-016-157096	Sequence 157096,	c 967	16	0.8	601	4	US-09-949-016-206535	Sequence 206535,
c 895	16	0.8	601	4	US-09-949-016-157097	Sequence 157097,	c 968	16	0.8	601	4	US-09-949-016-206535	Sequence 206535,
896	16	0.8	601	4	US-09-949-016-157482	Sequence 157482,	c 969	16	0.8	601	4	US-09-949-016-206535	Sequence 206535,
897	16	0.8	601	4	US-09-949-016-157589	Sequence 157589,	c 970	16	0.8	601	4	US-09-949-016-206535	Sequence 206535,
c 898	16	0.8	601	4	US-09-949-016-159077	Sequence 159077,	971	16	0.8	601	4	US-09-949-016-206535	Sequence 206535,
c 899	16	0.8	601	4	US-09-949-016-160640	Sequence 160640,	c 972	16	0.8	601	4	US-09-949-016-206535	Sequence 206535,
900	16	0.8	601	4	US-09-949-016-160641	Sequence 160641,	c 973	16	0.8	601	4	US-09-949-016-206535	Sequence 206535,
901	16	0.8	601	4	US-09-949-016-162744	Sequence 162744,	c 974	16	0.8	601	4	US-09-949-016-206535	Sequence 206535,
c 902	16	0.8	601	4	US-09-949-016-163039	Sequence 163039,	975	16	0.8	601	4	US-09-949-016-206535	Sequence 206535,
c 903	16	0.8	601	4	US-09-949-016-163040	Sequence 163040,	976	16	0.8	601	4	US-09-949-016-206535	Sequence 206535,

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977 16 0.8 723 4 US-09-489-039A-7101
c 978 16 0.8 733 3 US-09-392-184-15
979 16 0.8 745 4 US-10-101-464A-854
980 16 0.8 750 4 US-09-328-352-1248
c 981 16 0.8 753 4 US-09-702-705-1477
c 982 16 0.8 753 4 US-09-736-457-1477
c 983 16 0.8 753 4 US-09-614-124B-1477
c 984 16 0.8 753 4 US-09-671-1325-1477
c 985 16 0.8 753 4 US-09-658-824-1477
986 16 0.8 759 1 US-08-052-205-8
987 16 0.8 759 1 US-08-535-974-8
988 16 0.8 816 4 US-09-902-540-141
989 16 0.8 822 4 US-09-107-532A-1417
990 16 0.8 822 4 US-09-799-451-882
c 992 16 0.8 832 4 US-09-902-540-1979
c 993 16 0.8 832 4 US-09-270-767-5414
c 994 16 0.8 867 4 US-09-248-767-20696
c 995 16 0.8 868 3 US-09-248-768A-3191
c 996 16 0.8 882 4 US-08-961-527-262
997 16 0.8 882 4 US-09-252-991A-8694
998 16 0.8 886 1 US-08-469-427A-1
999 16 0.8 886 2 US-08-609-443B-1
1000 16 0.8 886 2 US-08-569-063C-1
Sequence 1, Appl1
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ALIGNMENTS

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RESULT 1
US-09-621-976-3396
; Sequence 3396, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; NUMBER OF SEQ ID NOS: 2000-07-21
; SOFTWARE: Patent.pm
; SEQ ID NO 3396
; LENGTH: 316
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 66..311
; NAME/KEY: misc_feature
; LOCATION: 301
; OTHER INFORMATION: n=a, y, c or t
US-09-621-976-3396
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Query Match 3.7%; Score 71; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 6.4e-24;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 143 CCACTCCAGGACCCCTCTCTCTCCATCCGAATACGAAGCTTCTCGACAGCGATC 202
DB 157 CCACTCCAGGACCCCTCTCTCTCCATCCGAATACGAAGCTTCTCGACAGCGATC 216
QY 203 CCACTCCAGGAG 213
DB 217 CCACTCCAGGAG 227
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RESULT 2
US-09-489-039A-6886
; Sequence 6886, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
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APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6886
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6886
Query Match 1.1%; Score 20; DB 4; Length 792;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
US-09-489-039A-7008
; Sequence 7008, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7008
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7008
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Query Match 1.1%; Score 20; DB 4; Length 1701;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1288 CTGTCCATCGGCAACCCAGGT 1307
DB 82 CTGTCCATCGGCAACCCAGGT 101
RESULT 4
US-07-745-206A-14/C
; Sequence 14, Application US/07745206A
; Patent No. 5429921
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: McCue, Ann
; APPLICANT: Feldman, Daniel
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: 135 S. LaSalle
; STREET: 135 S. LaSalle
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60603
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745,206A
FILING DATE: 19910815
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Feder, Scott B
REFERENCE/DOCKET NUMBER: 51504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2470 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2469
US-07-745-206A-14

Query Match 1.1%; Score 20; DB 1; Length 2470;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 701 AACAGGAAGCAAGAG 720
Db 1856 AACAGGAAGCAAGAG 1837

RESULT 5
US-08-311-363-14/c
Sequence 14, Application US/08311363
Patent No. 5876958
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,363
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999

TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2470 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2469
US-08-311-363-14

Query Match 1.1%; Score 20; DB 2; Length 2470;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 701 AACAGGAAGCAAGAG 720
Db 1856 AACAGGAAGCAAGAG 1837

RESULT 6
US-07-745-206A-12/c
Sequence 12, Application US/07745206A
Patent No. 5429921
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: McCue, Ann
APPLICANT: Feldman, Daniel
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 S. LaSalle
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745,206A
FILING DATE: 19910815
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Feder, Scott B
REFERENCE/DOCKET NUMBER: 51504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 5467 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(144..3164, 3168..3245, 3249..3386, 3390..3392, 3396..3488, 3495..3539, 3543..3581, 3585..3587, 3591..3626, 3630..3689, 3693..3737, 3744..3746, 3750..4823, 4827..4841, 4845..5006, 5010..5096, 5100..5306, 5310..5366, 5370..5465)
US-07-745-206A-12

Query Match 1.1%; Score 20; DB 1; Length 5467;

Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 701 AACAGAGAGCAGAGAG 720
DB 1999 AACAGAGAGCAGAGAG 1980

RESULT 7

US-08-311-363-12/c
; Sequence 12, Application US/08311363
; Patent No. 5876958
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,363
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-51506
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5467 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(144..3164, 3168..3245, 3249..3386, 3390
; ..3392, 3396..3488, 3495..3539, 3543..3581, 3585
; ..3587, 3591..3626, 3630..3689, 3693..3737, 3744
; ..3746, 3750..4823, 4827..4841, 4845..5006, 5010
; ..5096, 5100..5306, 5310..5366, 5370..5465)
US-08-311-363-12

Query Match 1.1%; Score 20; DB 2; Length 5467;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 701 AACAGAGAGCAGAGAG 720
DB 1999 AACAGAGAGCAGAGAG 1980

RESULT 8

US-08-456-200B-11/c
; Sequence 11, Application US/08456200B
; Patent No. 6229000
; GENERAL INFORMATION:
; APPLICANT: Franz, Jürgen, Weingartner, Bernhard;
; APPLICANT: Untereck, Axel, Rae, Peter
; TITLE OF INVENTION: TISSUE-SPECIFIC HUMAN NEURONAL
; TITLE OF INVENTION: CALCIUM CHANNEL SUB-TYPES AND
; TITLE OF INVENTION: THEIR USE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
; MEDIUM TYPE: Storage
; COMPUTER: NEC Powermate SX/20
; OPERATING SYSTEM: DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,200B
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/094,712
; FILING DATE: 19-JUL-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/858,278
; FILING DATE: 26-MAR-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/064,778
; FILING DATE: 19-MAY-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: DE 41 10 785
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 8398.3-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TEXT:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6232 nucleotides
; TYPE: Nucleotide
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: CDNA
US-08-456-200B-11

Query Match 1.1%; Score 20; DB 3; Length 6232;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 701 AACAGAGAGCAGAGAG 720
DB 887 AACAGAGAGCAGAGAG 868

RESULT 9

US-08-455-543A-8/c
; Sequence 8, Application US/08455543A
; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark

APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 144..6857
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..143
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 6855..7175
US-08-455-543A-8

Query Match 1.1%; Score 20; DB 1; Length 7175;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 701 AACAGGAAGCAAGAG 720
Db 1999 AACAGGAAGCAAGAG 1980

RESULT 10
US-08-193-078B-8/c
Sequence 8, Application US/08193078B
Patent No. 5846757
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWN, MARTIN, HALLER & MCCLAIN
STREET: 1660 UNION STREET
CITY: SAN DIEGO
STATE: CA
COUNTRY: USA
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,078B
FILING DATE: 07-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/868,354
FILING DATE: 10-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-53607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0062
TELEFAX: 619-238-0999
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 144..6857
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..143
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 6855..7175
US-08-193-078B-8

Query Match 1.1%; Score 20; DB 2; Length 7175;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 701 AACAGGAAGCAAGAG 720
|||||

Db 1999 AACAGGAAGCAGAGAAGAG 1980

RESULT 11

US-08-223-305C-8/c

Sequence 8, Application US/08223305C

Patent No. 5851824

GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark

APPLICANT: Feldman, Daniel

APPLICANT: McCue, Ann

APPLICANT: Brenner, Robert

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/223,305C

FILING DATE: April 4, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/868,354

FILING DATE: April 10, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745,206

FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/620,250

FILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/482,384

FILING DATE: 20-FEB-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/603,751

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US89/01408

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/176,899

FILING DATE: 04-APR-1988

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 52516 (P519739)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619)238-0399

TELEFAX: (619)238-0062

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 7175 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 144..6857

FEATURE:

NAME/KEY: 5'UTR

LOCATION: 1..143

FEATURE:

NAME/KEY: 3'UTR

LOCATION: 685..7175

US-08-223-305C-8

Query Match 1.1% Score 20; DB 2; Length 7175;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 701 AACAGGAAGCAGAGAAGAG 720

Db 1999 AACAGGAAGCAGAGAAGAG 1980

RESULT 12

US-08-149-097D-8/c

Sequence 8, Application US/08149097D

Patent No. 5874236

GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark

APPLICANT: Feldman, Daniel

APPLICANT: McCue, Ann

APPLICANT: Brenner, Robert

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/149,097D

FILING DATE: 05-NOV-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/105,536

FILING DATE: 11-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US92/06903

FILING DATE: 14-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/914,231

FILING DATE: 13-JUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/868,354

FILING DATE: 10-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745,206

FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/620,250

FILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/482,384

FILING DATE: 20-FEB-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/603,751

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US89/01408

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/176,899

FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-55038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 238-0099
TELEFAX: (619) 238-0062
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 144..6857
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..143
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 6855..7175
US-08-149-097D-8

Query Match 1.1%; Score 20; DB 2; Length 7175;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 701 AACGAGAGCAAGAG 720
Db 1999 AACGAGAGCAAGAG 1980

RESULT 13
US-08-949-386-8/c
Sequence 8, Application US/08949386
Patent No. 6090623
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: McCue, Ann
APPLICANT: Gillespie, Alison
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: US
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/949,386
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/290,012
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 08/149,097
FILING DATE: 5-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,536
FILING DATE: 11-AUG-1993
ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 519808
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 238-0099
TELEFAX: (619) 238-0062
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 144..6857
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..143
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 6855..7175
US-08-949-386-8

Query Match 1.1%; Score 20; DB 3; Length 7175;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 701 AACGAGAGCAAGAG 720
Db 1999 AACGAGAGCAAGAG 1980

RESULT 14
US-08-450-562-8/c
Sequence 8, Application US/08450562
Patent No. 6096514
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: McCue, Ann
APPLICANT: Gillespie, Alison
APPLICANT: Feldman, Daniel
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: US
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,562
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/404,950
FILING DATE: 13-MAR-1995
APPLICATION NUMBER: 08/336,257
FILING DATE: 7-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/314,083
FILING DATE: 28-SEPT-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/311,363
FILING DATE: 23-SEPT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,012
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: 4-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/193,078
FILING DATE: 07-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/149,097
FILING DATE: 5-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,536
FILING DATE: 11-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/914,231
FILING DATE: 13-JULY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: 10-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06903
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/603,751
FILING DATE: 08-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/482,384
FILING DATE: 02-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-519812
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 238-0999
TELEFAX: (619) 238-0062
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 144..6857
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..143
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 6855..7175
US-08-450-562-8

Query Match 1.1%; Score 20; DB 3; Length 7175;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 701 AACAGGAAGCAAGAG 720
Db 1999 AACAGGAAGCAAGAG 1980

RESULT 15
US-08-984-709A-8/C
Sequence 8, Application US/08984709A
Patent No. 6320032
GENERAL INFORMATION:
APPLICANT: Williams, Mark E.
APPLICANT: Stauderman, Kenneth A.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Heller Ehrman White & McLaughlin
STREET: 4250 Executive Square, Suite 700
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,709A
FILING DATE: 02-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 450-8400
TELEFAX: (619) 587-5360
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 144..6857
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..143
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 6855..7175
US-08-984-709A-8

Query Match 1.1%; Score 20; DB 3; Length 7175;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 701 AACAGGAAGCAAGAG 720
Db 1999 AACAGGAAGCAAGAG 1980

Search completed: March 8, 2005, 01:45:00
Job time : 373 secs